Docket No. 50950/JPW/EMW

June 29, 2000

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Honorable Assistant Commissioner for Patents
Washington, D.C. 20231

S I R:

Transmitted herewith for filing are the specification and claims of the patent application of:

Wayne A. Hendrickson et al. for
Inventor(s)

CONJUGATED LIGANDS FOR THE STIMULATION OF BLOOD CELL PROLIFERATION BY EFFECTING DIMERIZATION OF THE RECEPTOR FOR STEM CELL FACTOR
Title of Invention

Also enclosed are:

X 85 sheet(s) of ____informal X formal drawings.

X Oath or declaration of Applicant(s). (unsigned)

X A power of attorney

____ An assignment of the invention to _____

____ A Preliminary Amendment

X A verified statement to establish small entity status under 37 C.F.R. §1.9 and §1.27. (unsigned)

The filing fee is calculated as follows:

CLAIMS AS FILED, LESS ANY CLAIMS CANCELLED BY AMENDMENT

	NUMBER FILED		NUMBER EXTRA*		RATE SMALL ENTITY	RATE OTHER ENTITY		FEE SMALL ENTITY	FEE OTHER ENTITY
Total Claims	47 -20	=	27	X	$ 9.00	$18.00	=	$ 243.00	$
Independent Claims	4 -3	=	1	X	$39.00	$78.00	=	$ 9.00	$
Multiple Dependent Claims Presented: ____Yes X No					$130.00	$260.00	=	$ 0	$
						BASIC FEE		$ 345	$ 690
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X A check in the amount of $ 627.00 to cover the filing fee.

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X The Commissioner is hereby authorized to charge any additional fees which may be required in connection with the following or credit any over-payment to Account No. 03-3125:

X Filing fees under 37 C.F.R. §1.16.

X Patent application processing fees under 37 C.F.R. §1.17.

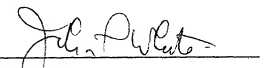
____ The issue fee set in 37 C.F.R. §1.18 at or before mailing of the Notice of Allowance, pursuant to 37 C.F.R. §1.311(b).

X Three copies of this sheet are enclosed.

____ A certified copy of previously filed foreign application No. _____ _____ filed in _____ on _____. Applicant(s) hereby claim priority based upon this aforementioned foreign application under 35 U.S.C. §119.

X Other (identify) Express Mail Certificate of Mailing bearing no. EL 807 507 584 US dated June 29, 2000, a loose set of figures (85 sheets), paper copy of Sequence Listing, CRF of Sequence Listing, and Statement in Accordance.

Respectfully submitted,



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Applicant or Patentee: Wayne A. Hendrickson et al.
Serial or Patent No.: Not Yet Known
Filed or Issued: Herewith
Attorney's Docket No: 50950/JPW/EMW
Title of Invention or Patent: CONJUGATED LIGANDS FOR THE STIMULATION OF BLOOD CELL PROLIFERATION BY EFFECTING DIMERIZATION OF THE RECEPTOR FOR STEM CELL FACTOR

VERIFIED STATEMENT (DECLARATION) CLAIMING
SMALL ENTITY STATUS UNDER 37 C.F.R. §1.9(f)
AND §1.27(d) - NONPROFIT ORGANIZATION

I hereby declare that I am an official empowered to act on behalf of the nonprofit organization identified below:

Name of Organization: The Trustees of Columbia University in the City of New York

Address of Organization: West 116th Street and Broadway
New York, New York 10027

TYPE OF ORGANIZATION:

__X__ UNIVERSITY OR OTHER INSTITUTION OF HIGHER EDUCATION
TAX EXEMPT UNDER INTERNAL REVENUE SERVICE CODE 26 U.S.C. §§501(a) and 501(c)(3)

_____ NONPROFIT SCIENTIFIC OR EDUCATIONAL UNDER STATUTE OF STATE OF THE UNITED STATES OF AMERICA
NAME OF STATE: _____
CITATION OF STATUTE: _____

_____ WOULD QUALIFY AS TAX EXEMPT UNDER INTERNAL REVENUE SERVICE CODE 26 U.S.C. §§501(a) and 501(c)(3) IF LOCATED IN THE UNITED STATES OF AMERICA

_____ WOULD QUALIFY AS NONPROFIT SCIENTIFIC OR EDUCATIONAL UNDER STATUTE OF STATE OF THE UNITED STATES OF AMERICA IF LOCATED IN THE UNITED STATES OF AMERICA
NAME OF STATE: _____
CITATION OF STATUTE: _____

I hereby declare that the nonprofit organization identified above qualifies as a nonprofit organization as defined in 37 C.F.R. §1.9(e)* for purposes of paying reduced fees under 35 U.S.C. §41(a) and 41(b), with regard to the invention entitled CONJUGATED LIGANDS FOR THE STIMULATION OF BLOOD CELL PROLIFERATION BY EFFECTING DIMERIZATION OF THE RECEPTOR FOR STEM CELL FACTOR
by inventor(s) Wayne A. Hendrickson et al.

described in:

__X__ the specification filed herewith
_____ application serial no. _____ filed _____
_____ patent no. _____ issued _____

I hereby declare that rights under contract or law have been conveyed to and remain with the nonprofit organization with regard to the above identified invention.

If the rights held by the nonprofit organization are not exclusive each individual, concern, or organization known to have rights to the invention is listed below[a] and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 C.F.R. §1.9(d)* or a nonprofit organization under 37 C.F.R. 1.9(e)*

[a]NOTE: Separate verified statements are required from each person, concern, or organization having rights to the invention averring to their status as small entities. 37 C.F.R. §1.27.

Name: N/A
Address: _____

____Individual ____ Small Business Concern ____Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. 37 C.F.R. §1.28(b)*.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. §1001, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Name of Person Signing: Mr. Jack M. Granowitz
Title In Organization: Executive Director, Columbia Innovation Enterprise
Address: Amsterdam & 120th Street - Suite 363 New York, New York 10027

Signature: _____
Date Of Signature: _____

*See Reverse

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Bar Seq

Dkt. 50950/JPW/EMW

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants	:	Wayne A. Hendrickson et al.
U.S. Serial No.	:	Not Yet Known
Filed	:	Herewith
For	:	CONJUGATED LIGANDS FOR THE STIMULATION OF BLOOD CELL PROLIFERATION BY EFFECTING DIMERIZATION OF THE RECEPTOR FOR STEM CELL FACTOR

1185 Avenue of the Americas
New York, New York 10036
June 29, 2000

Assistant Commissioner for Patents
Washington, D.C. 20231

Box: Patent Application

EXPRESS MAIL CERTIFICATE OF MAILING
FOR ABOVE-IDENTIFIED APPLICATION

"Express Mail" mailing label number: EJ 807 507 584 US
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I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. §1.10 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

Signature: Elizabeth M. Wierzkowski
Printed Name: ELIZABETH M. WIERZKOWSKI

Respectfully submitted,

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Application
for
United States Letters Patent

To all whom it may concern:

Be it known that we, Wayne A. Hendrickson, Xuliang Jiang, Keith E. Langley, Rashid Syed and Yueh-Rong Ann Hsu

have invented certain new and useful improvements in

CONJUGATED LIGANDS FOR THE STIMULATION OF BLOOD CELL PROLIFERATION BY EFFECTING DIMERIZATION OF THE RECEPTOR FOR STEM CELL FACTOR

of which the following is a full, clear and exact description.

CONJUGATED LIGANDS FOR THE STIMULATION OF BLOOD CELL PROLIFERATION BY EFFECTING DIMERIZATION OF THE RECEPTOR FOR STEM CELL FACTOR

Throughout this application, various references are referred to within parentheses. Disclosures of these publications in their entireties are hereby incorporated by reference into this application to more fully describe the state of the art to which this invention pertains. Full bibliographic citation for these references may be found at the end of this application, preceding the claims.

Field of the Invention

This invention relates to stem cell factor (SCF) analogs, compositions containing such analogs, and related compositions. In another aspect, the present invention relates to nucleic acids encoding the present analogs or related nucleic acids, related host cells and vectors. In another aspect, the invention relates to computer programs and apparatuses for expressing the three dimensional structure of SCF and analogs thereof. In another aspect, the invention relates to methods for rationally designing SCF analogs and related compositions. In yet another aspect, the present invention relates to methods for treatment using the present SCF analogs.

BACKGROUND OF THE INVENTION

Stem cell factor (SCF) is an early-acting hematopoietic cytokine which elicits multiple biological effects. SCF is dimeric and occurs in soluble and membrane-bound forms. It transduces signals by ligand-mediated dimerization of its receptor, Kit. Kit is a receptor tyrosine kinase related to the receptors for platelet-derived growth factor (PDGF) and to those for vascular endothelial growth factor (VEGF), fibroblast growth factor (FGF), macrophage colony-stimulating factor (M-CSF) and Flt-3 ligand. The kinase portions of these receptors are closely related and their ligand-binding portions all comprise immunoglobulin-like (Ig) repeats, although these vary widely in sequence and also in number. Determined here is the crystal structure of selenomethionyl soluble human SCF at 2.2 Å resolution by multiwavelength anomalous diffraction (MAD) phasing. SCF has the characteristic helical cytokine topology, but the structure is unique apart from core portions. The SCF dimer has a symmetric 'head-to-head' association. Potential Kit-binding sites on the SCF dimer surface are located. A superposition of this dimer onto VEGF in its complex with the Flt-1 receptor places the binding sites on SCF in positions of topographical and electrostatic complementarity with the Kit counterparts of Flt-1. Similar models can be made for the complex of PDGF with its receptor and FGF-heparin.

INTRODUCTION

Stem cell factor (SCF) is an early-acting hematopoietic

cytokine that binds at the cell surface to its receptor, Kit, whereby it produces other biological effects in addition to those on hematopoiesis (see reviews by Galli et al., 1994; Lev et al., 1994; Besmer et al., 1997; Broudy, 1997). SCF, which is produced by various fibroblast-type cells including bone marrow stromal cells, has also been called Kit ligand (KL), mast-cell growth factor (MGF), and steel factor. The biochemistry and molecular biology that identified SCF and Kit as a ligand-receptor pair were preceded by an array of elegant animal biology studies that anticipated the underlying molecular mechanisms responsible for the genetics (Russell, 1979). Mice with mutations in the *Sl* locus (gene for SCF) or in the dominant-spotting *W* locus (*c-kit, the* gene for Kit) show complex phenotypes that include macrocytic anemia, sterility from a deficiency of germ cells, lack of coat pigmentation (white spotting of the skin from absences of pigment cells) and mast cell deficiency. Kit mutations in man are responsible for the autosomal dominant congenital pigmentation disorder, piebaldism. Consistent with these phenotypes, in the last 10 years, a host of *in vitro* and *in vivo* experiments have clearly established Kit-mediated roles for SCF in early stages of hematopoiesis, in gametogenesis, in melanocyte proliferation and function and in mast cell proliferation, maturation and activation; (Galli *et al.*, 1994, Lev et al., 1994, Besmer et al., 1997; Broudy, 1997). SCF has potential therapeutic applications in the treatment of anemias, boosting the mobilization of hematopoietic stem/ progenitor cells to the peripheral blood for harvest and transplantation, and in increasing

the efficiency of gene transduction for gene therapy (Galli *et al.*, 1994, McNiece and Briddell, 1995, Glaspy, 1996, Broudy, 1997).

SCF is expressed as membrane-associated forms of either 248 or 220 amino acid residues (Galli *et al.*, 1994, Lev et al., 1994, Besmer et al., 1997, Broudy, 1997) The two forms are a consequence of alternative mRNA splicing that includes or excludes exon 6. Exon 6 encodes a proteolytic cleavage site such that soluble SCF^{1-165} is released from the 248 amino-acid precursor. Residues 166-189 represent a tether to the membrane, residues 190-221 represent a hydrophobic transmembrane segment, and residues 222-248 represent a cytoplasmic domain. The 220 amino acid residue form lacks the cleavage site and tends to remain membrane-bound. Soluble SCF exists as a non-covalently associated dimer (Arakawa *et al.*, 1991). Each SCF monomer contains two intra-chain disulfide bridges, Cys4-Cys 89 and Cys43-Cys138 (Langley et al, 1992). The N-terminal 141 residues of SCF have been identified as a functional core, SCF^{1-141}, that includes the dimer interface and portions that bind and activate the receptor Kit (Langley *et al.*, 1994).

It has been proposed that SCF is a member of the helical cytokine structural superfamily characterized by a double-crossover four-helix bundle topology (Bazan, 1991). Three-dimensional structures are known for many of the family members and, from a comparison of the structures and sequences, the members have been classified into three subgroups (Sprang and Bazan, 1993):

short-chain, long-chain and interferon-like.

The superfamily is highly divergent. Among five short-chain helical cytokines of known structure, sequence identity levels rarely exceed 20% and fewer than half of the residues constitute (41%-48%) a common framework of the fold with r.m.s. deviations ranging from 1.7 Å to 2.9Å for the 61 C_α positions in common. Furthermore, many identical residues adopt different side chain conformations in the various structures. Nevertheless, sequence patterns do persist from the secondary structure and SCF has been proposed to be a short-chain helical cytokine (Bazan, 1991; Rozwarski *et al.*, 1994).

Most helical cytokines signal through members of the hematopoietic cytokine receptor superfamily, which are without intrinsic kinase activity (Heldin, 1995). SCF, in contrast, signals through a class III receptor tyrosine kinase (i.e. Kit). This class of kinases also includes the receptors for platelet-derived growth factor (PDGF), macrophage colony-stimulating factor (M-CSF), granulocyte-macrophage colony-stimulating factor (GM-CSF), and Flt-3 ligand, and it is related to class V receptor tyrosine kinases (Flt-1, Flt-1/KDR and Flt-4) for vascular endothelial growth factors (VEGFs) (Fantl et al., 1993; Heldin, 1995; Rousset et al., 1995). The receptors in these classes have 'split' kinase domains intracellularly and multiple immunoglobulin(Ig)-like domains extracellularly.

The structures of PDGF (Oefner *et al.*, 1992), M-CSF (Pandit *et al.*, 1992), and VEGF (Muller *et al.*, 1997), have all been determined by X-ray crystallography, as has the complex of VEGF with domain 2 of its receptor, Flt-1 (Wiesmann *et al.*, 1997).

The ligands for the class III and class V receptors are all dimeric. As is the case for other ligands, SCF initiates signal transduction by dimerization of its receptor, Kit and the two juxtaposed receptors undergo tyrosine autophosphorylation (Heldin, 1995; Broudy, 1997), which initiates downstream intracellular signaling.

Here reported is the crystal structure of the core fragment of recombinant human stem cell factor, SCF^{1-141}, as determined at 2.2 Å resolution from multiwavelength anomalous diffraction (MAD) measurements. Incorporating data from mutagenesis and other structure-function studies, located were putative receptor-binding sites on the surface of the symmetric SCF dimer. From a comparison of these results with the structural and functional data for the related ligand-receptor systems, the complex of SCF with the receptor Kit is modeled and suggests a similar mode of association between other class III and class V receptors and their ligands.

Human SCF can be obtained and purified from a number of sources. SCF has been isolated from the rat and the mouse. Using the amino acid sequence of SCF protein isolated from the rat, the nucleic acid sequence encoding

the rat protein sequence was obtained from a rat cDNA library and then was cloned. The cloned nucleic acid encoding rat SCF was used to isolate, by hybridization, the nucleic acid molecule encoding human SCF from a human cDNA library. The development of recombinant DNA technology, see, for instance, U.S. Patent 4,810,643 (Souza) incorporated herein by reference, has enabled the production of commercial scale quantities of SCF in glycosylated form as a product of eukaryotic host cell expression, and of SCF in non-glycosylated form as a product of prokaryotic host cell expression.

SUMMARY OF THE INVENTION

The three dimensional structure of SCF has been determined herein to the atomic level. From this three-dimensional structure, one can now forecast with substantial certainty how changes in the composition of a SCF molecule may result in structural changes. These structural characteristics may be correlated with biological activity to design and produce SCF analogs.

This invention provides a computer based method for preparing a stem cell factor (SCF) analog comprising the steps of: (a) providing computer expression of the three dimensional structure of an SCF molecule using its crystal structure; (b) selecting from the computer expression of step (a) at least one site on the SCF molecule for alteration; (c) preparing an SCF molecule having an alteration at said at least one selected site; and (d) optionally, testing the SCF molecule for a desired characteristic.

This invention also provides an isolated SCF analog prepared according to the above-described computer based method for preparing a stem cell factor (SCF) analog comprising the steps of: (a) providing computer expression of the three dimensional structure of an SCF molecule using its crystal structure; (b) selecting from the computer expression of step (a) at least one site on the SCF molecule for alteration; (c) preparing a SCF molecule having an alteration at said at least one selected site; and (d) optionally, testing the SCF

molecule for a desired characteristic. In an embodiment the above-described SCF analog binds to SCF receptor, Kit. As used herein SCF receptor and "Kit" are used interchangeably to reflect the varied nomenclature used in the art.

This invention provides a composition comprising an isolated SCF analog prepared according to the above-described computer based method for preparing a stem cell factor (SCF) analog comprising the steps of: (a) providing computer expression of the three dimensional structure of an SCF molecule using its crystal structure; (b) selecting from the computer expression of step (a) at least one site on the SCF molecule for alteration; (c) preparing a SCF molecule having an alteration at said at least one selected site; and (d) optionally, testing the SCF molecule for a desired characteristic, effective to treat a subject and a pharmaceutically acceptable carrier.

This invention provides a method of treating a subject comprising administration of an isolated SCF analog prepared by the above-described computer based method for preparing a stem cell factor (SCF) analog comprising the steps of: (a) providing computer expression of the three dimensional structure of an SCF molecule using its crystal structure; (b) selecting from the computer expression of step (a) at least one site on the SCF molecule for alteration; (c) preparing a SCF molecule having an alteration at said at least one selected site; and (d) optionally, testing the SCF molecule for a

desired characteristic.

This invention provides a method for designing a compound (drug) capable of binding to the receptor of stem cell factor (SCF), Kit, comprising the steps of: a) determining a receptor binding site on the SCF based on the three dimensional structure of SCF or an SCF polypeptide **capable of binding the receptor; and b) designing a compound comprising an entity that binds the SCF receptor.** Accordingly, the designed compound is an SCF ligand analog, since a portion or part of the compound, "the entity", mimics the portion of SCF that binds to the SCF receptor, Kit. In step (a), and infra, the receptor binding site may be determined from atomic coordinates computed from X-ray diffraction data of a crystal comprising a polypeptide having an amino acid sequence portion of SCF capable of binding the receptor.

This invention provides a compound designed by the above-described method for designing a compound capable of binding to the receptor site of stem cell factor (SCF), Kit, comprising the steps of: a) determining a receptor binding site, on the SCF based on the atomic coordinates computed from X-ray diffraction data of a crystal comprising a polypeptide having an amino acid sequence portion of SCF capable of binding a ligand; and b) designing a **compound comprising an entity that binds the SCF receptor. As used herein, the entity, i,.e. the portion, of the designed compound fits the ligand binding site on the SCF receptor.**

This invention provides a method of treating a subject comprising administration of a compound designed by the above-described method for designing a compound capable of binding to the SCF receptor site.

This invention also provides a method of stimulating the production of hematopoietic calls in a subject comprising administering an isolated stem cell factor (SCF) analog or SCF ligand analogs to the subject.

This invention provides an isolated stem cell factor (SCF) molecule, which is an altered SCF, comprising any portion of amino acids 1-165 of a human SCF polypeptide, optionally comprising an N-terminal methionine before amino acid residue 1, wherein the polypeptide has an amino acid sequence portion of SCF capable of binding to the SCF receptor, Kit. Amino acid residue 1 of SCF is E, glutamic acid.

BRIEF DESCRIPTION OF THE FIGURES

Figures 1A-1C. Representative electron-density distributions in SCF. (Fig. 1A) MAD-phased experimental map calculated at 2.3 Å resolution. (Fig. 1B) The experimental map after four-fold averaging. (Fig. 1C) The current $2F_o$-F_c map superimposed with the model refined at 2.2 Å resolution. Each map is contoured at 1.0σ. Figures were drawn by the program O (Jones *et al.*, 1991).

Figures 2A-2B. Overall structure of an SCF dimer. (Fig. 2A) Ribbon diagram. (Fig. 2B) C_α stereodiagram of the AB dimer. Figures were drawn using the program SETOR (Evans, 1993).

Figure 3. Structure-based sequence alignment of SCF with other short-chain helical cytokines of human species. The dots denote gaps. M-CSF, IL-4, GM-CSF, IL-2 and IL-5 were aligned with SCF structure through structural superposition using TOSS (Hendrickson, 1979) and O (Jones *et al.*, 1991). C_α atoms were included if within 3.0 Å of their counterparts after superposition and at least three consecutive such residues are found in the fragment. The secondary structure

elements were assigned according to the output of the PROCHECK program (Laskowski *et al.*, 1993) except the helix assignment for residues 35-38, which was identified by inspection of the hydrogen-bond pattern. Secondary structures are shown in yellow with filled boxes referring to α-helices, half-filled boxes to 3_{10}-helices and arrows to β-strands. The solvent accessibility of the SCF dimer is indicated for each residue by an open circle if the fractional solvent accessibility is ›0.4, a half-filled circle if it is 0.1-0.4, and a filled circle if it is ‹0.1. Residues at the SCF dimer interface are identified by stars, and the N-linked glycosylation sites by red Ys above the Asn residues.

Figures 4A-4B. Comparison of SCF dimer (shades of green) and M-CSF dimer (shades of brown). (Fig. 4A) View as in Figure 2. (Fig. 4B) View perpendicular to Fig. 4A, along the diad axis of M-CSF. Symmetry axes are shown as lines in Fig. 4A and dots in Fig. 4B. When one subunit of SCF dimer is superimposed onto a subunit of the M-CSF dimer, the other subunits are translated by 3.8 Å with a rotation of 4.7° to each other. Figures were generated using the program GRASP (Nicholls *et al.*, 1991).

Figure 5. Sequence alignments of SCF from human, mouse, rat and dog. (Anderson et al., 1990; Huang et al., 1990; Martin et al. 1990; Shull et al., 1992) The residues that are conserved in human and dog but different from rat and mouse are shadowed in yellow. Five regions of divergent sequence are identified (Roman numerals) Dots denote gaps, and dashes indicate residues identical to the human residues.

Figures 6A-6C. Ligand (worm structures)-receptor (yellow structures) models. (Fig. 6A) VEGF-Flt-1. (Fig. 6B) SCF-Kit. (Fig. 6C) PDGF-{DGF receptor. The used, without any modification, to approximate the receptor models. Receptor models are presented as yellow surfaces. The ligand models are presented as worm models. Background portions are colored light blue for one monomer and green for the other; receptor-interacting residues identified from site-directed mutagenesis experiments [VEGF (Muller et al.,1997), PDGF (Fenstermaker et al., 1993)] and other experimental data (SCF; see infra) arecolored magenta. Figures were drawn by the program GRASP (Nicholls *et al.*, 1991).

Figures 7A-7C. Electrostatic and carbohydrate surfaces of SCF and homology-modeled receptor Kit. (Fig. 7A) Electrostatic surface of SCF and worm of D2D3(Kit). (Fig. 7B) Electrostatic surface of Kit and worm of SCF. **(Fig. 8C)** Negative potential is colored red and positive potential, blue, with greatest saturations at -10 and +10kT, respectively. Carbohydrate moieties are represented by CPK models of a β-D-N-acetylglucose (green for SCF moieties and yellow for potential Kit moieties. Figures were drawn by the program GRASP (Nicholls *et al.*, 1991).

Figure 8. X-ray crystallographic coordinates of truncated stem cell factor molecule comprising amino acids 1-141 of a human SCF polypeptide.

Figure 9. Suggested renaming of the waters of the X-ray crystallographic coordinates set forth in Figure 8.

Figure 10. Design for a double-headed SCF ligand analog. (10A) General model (10B) Embodiment of the ligand head as an oligopeptide. The compound is the conjugation of a linker molecule with two ligand-head molecules. Each ligand head

is composed of up to three functional moieties, F_1, F_2 and F_3, which serve to mimic receptor-binding sites on the surface of SCF. Each ligand head also contains a conjugation moiety, F_L, endowed with chemical reactivity for conjugation with a reactive group at the end of the linker molecule. The capping moiety, F_C, at each end of the linker molecule is endowed with chemical reactivity for conjugation with the conjugation moiety from the ligand head. Double-headed molecules of this structure can have the property of binding to the SCF receptor, Kit, in such a way as to dimerize the receptor molecules and thereby lead to Kit activation in a manner analogous to the natural activity of SCF.

Ligand heads can be designed in at least four ways. (1) Ligand heads can be synthesized as oligopeptides wherein the functional moieties (F_1, F_2, F_3) are sequence elements from the SCF polypeptide; (2) The functional moieties (F_1, F_2, F_3) on such a ligand head can be selected by bacteriophage display for optimal receptor binding; (3) Chemical mimetics of the functional moieties and connecting segments in an active oligopeptide can be substituted for the respective moieties and segments; or (4)

An appropriate chemical framework (scaffold) of connecting segments can be designed to present functional moieties (F_1, F_2, F_3) which can be selected by combinatorial chemistry for optimal receptor binding from a library of chemical moieties complementary to receptor-binding sites on the surface of SCF.

When an oligopeptide embodiment of a linker head is designed in accord with option (1) it can have a sequence wherein F_1 corresponds to a segment from within the N-terminal region of SCF, residues 1-10; F_2 corresponds to a segment from within residues 79-95 (mainly located on the αC helix); F_3 is a segment from the C-terminal end of αD, near residue 127; F_L is a cysteine residue; and X_n, X_m, and X_p are connecting-peptide segments, composed from appropriate linker residues such as alanine, glycine, serine or proline, and wherein n=0-5, m=0-5 and p=3-8 residues, respectively.

Linkers can be designed from an organic polymer such as polyethylene glycol $H[OCH_2CH_2]_nOH$, where n=10-20 may suffice to separate the heads appropriately, wherein a reactive capping moiety, F_C, is appended at each end. The capping moiety may be a thiol reactive group, such as N-ethyl

maleimide, designed to bond covalently to the conjugation moiety, F_L, on the ligand head, wherein F_L may be cysteine residue or another thiol-containing group.

DETAILED DESCRIPTION OF THE INVENTION

The present determination of the three-dimensional structure to the atomic level is the most complete analysis to date, and provides important information to those wishing to design and prepare SCF analogs. For example, from the present three dimensional structural analysis, precise areas of hydrophobicity and hydrophilicity have been determined.

Relative hydrophobicity is important because it directly relates to the stability of the molecule. Generally, biological molecules, found in aqueous environments, are externally hydrophilic and internally hydrophobic; in accordance with the second law of thermodynamics provides, this is the lowest energy state and provides for stability. Although one could have speculated that SCF's internal core would be hydrophobic, and the outer areas would be hydrophilic, one would have had no way of knowing specific hydrophobic or hydrophilic areas. With the presently provided knowledge of areas of hydrophobicity/-philicity, one may forecast with substantial certainty which changes to the SCF molecule will affect the overall structure of the molecule.

As a general rule, one may use knowledge of the geography of the hydrophobic and hydrophilic regions to design analogs in which the overall SCF structure is not changed, but change does affect biological activity ("biological activity" being used here in its broadest sense to denote function). One may correlate biological

activity to structure. If the structure is not changed, and the mutation has no effect on biological activity, then the mutation has no biological function. If, however, the structure is not changed and the mutation does affect biological activity, then the residue (or atom) is essential to at least one biological function. Some of the present working examples were designed to provide no change in overall structure, yet have a change in biological function.

Based on the correlation of structure to biological activity, one aspect of the present invention relates to SCF analogs. These analogs are molecules which have more, fewer, different or modified amino acid residues from the SCF amino acid sequence. The modifications may be by addition, substitution, or deletion of one or more amino acid residues. The modification may include the addition or substitution of analogs of the amino acids themselves, such as peptidomimetics or amino acids with altered moieties such as altered side groups. The SCF used as a basis for comparison may be of human, animal or recombinant nucleic acid-technology origin (although the working examples disclosed herein are based on the recombinant production of the 141 amino acid species of human SCF, optionally having an extra N-terminal methionine residue). The analogs may possess functions different from natural human SCF molecule, or may exhibit the same functions, or varying degrees of the same functions. For example, the analogs may be designed to have a higher or lower biological activity, have a longer shelf-life or a decrease in stability, be easier to

formulate, or more difficult to combine with other ingredients. The analogs may bind receptor but elicit no biological activity and may therefore be useful as an antagonist against SCF effect (as, for example, in the overproduction of SCF). From time to time herein the present analogs are referred to as proteins or peptides for convenience, but contemplated herein are other types of molecules, such as peptidomimetics or chemically modified peptides.

In embodiment, the present invention relates to related compositions containing a SCF analog as an active ingredient. The term, "related composition," as used herein, is meant to denote a composition which may be obtained once the identity of the SCF analog is ascertained (such as a SCF analog labeled with a detectable label or pharmaceutical composition). Also considered a related composition are chemically modified versions of the SCF analog, such as those having attached at least one polyethylene glycol molecule.

For example, one may prepare a SCF analog to which a detectable label is attached, such as a fluorescent, chemiluminescent or radioactive molecule.

Another example is a pharmaceutical composition which may be formulated by known techniques using known materials, see, e.g., Remington's Pharmaceutical Sciences, 18th Ed. (1990, Mack Publishing Co., Easton, Pennsylvania 18042) pages 1435-1712, which are herein incorporated by reference. Generally, the formulation will depend on a

variety of factors such as administration, stability, production concerns and other factors. The SCF analog may be administered by injection or by pulmonary administration via inhalation. Enteric dosage forms may also be available for the present SCF analog compositions, and therefore oral administration may be effective. SCF analogs may be inserted into liposomes or other microcarriers for delivery, and may be formulated in gels or other compositions for sustained release. Although preferred compositions will vary depending on the use to which the composition will be put, generally, for SCF analogs having at least one of the biological activities of natural SCF, preferred pharmaceutical compositions are those prepared for subcutaneous injection or for pulmonary administration via inhalation, although the particular formulations for each type of administration will depend on the characteristics of the analog.

Another example of related composition is a receptor for the present analog. As used herein, the term "receptor" indicates a moiety which selectively binds to the present analog molecule. For example, antibodies, or fragments thereof, or "recombinant antibodies" (see Huse et al., Science 246:1275 (1989)) may be used as receptors. Selective binding does not mean only specific binding (although binding-specific receptors are encompassed herein), but rather that the binding is not a random event. Receptors may be on the cell surface or intra- or extra-cellular, and may act to effectuate, inhibit or localize the biological activity of the present analogs.

Receptor binding may also be a triggering mechanism for a cascade of activity indirectly related to the analog itself. Also contemplated herein are nucleic acids, vectors containing such nucleic acids and host cells containing such nucleic acids which encode such SCF analogs.

Another example of a related composition is a SCF analog with a chemical moiety attached. Generally, chemical modification may alter biological activity or antigenicity of a protein, or may alter other characteristics, and these factors will be taken into account by a skilled practitioner. As noted above, one example of such chemical moiety is polyethylene glycol. Modification may include the addition of one or more hydrophilic or hydrophobic polymer molecules, fatty acid molecules, or polysaccharide molecules. Examples of chemical modifiers include polyethylene glycol, alklpolyethylene glycols, DI-poly(amino acids), polyvinylpyrrolidone, polyvinyl alcohol, pyran copolymer, acetic acid/acylation, proprionic acid, palmitic acid, lecithin, stearic acid, dextran, carboxymethyl cellulose, pullulan, or agarose. See, Francis, *Focus on Growth Factors* 3: 4-10 (May 1992)(published by Mediscript, Mountview Court, Friern Barnet Lane, London N20 OLD, UK). Also, chemical modification may include an additional protein or portion thereof, use of a cytotoxic agent, or an antibody.

In another embodiment, the present invention relates to nucleic acids encoding such analogs. The nucleic acids

may be DNAs or RNAs or derivatives thereof, and will typically be cloned and expressed on a vector, such as a phage or plasmid containing appropriate regulatory sequences. The nucleic acids may be labeled (such as using a radioactive, chemiluminescent, or fluorescent label) for diagnostic or prognostic purposes, for example. The nucleic acid sequence may be optimized for expression, such as including codons preferred for bacterial expression. The nucleic acid and its complementary strand, and modifications thereof which do not prevent encoding of the desired analog are here contemplated.

In another embodiment, the present invention relates to host cells containing the above nucleic acids encoding the present analogs. Host cells may be eukaryotic or prokaryotic, and expression systems may include extra steps relating to the attachment (or prevention) of sugar groups (glycosylation), proper folding of the molecule, the addition or deletion of leader sequences or other factors incident to recombinant expression.

In further embodiment the present invention relates to antisense nucleic acids which act to prevent or modify the type or amount of expression of such nucleic acid sequences. These may be prepared by known methods.

In another embodiment of the present invention, the nucleic acids encoding a present analog may be used for gene therapy purposes, for example, by placing a vector containing the analog-encoding sequence into a recipient

so the nucleic acid itself is expressed inside the recipient who is in need of the analog composition. The vector may first be placed in a carrier, such as a cell, and then the carrier placed into the recipient. Such expression may be localized or systemic. Other carriers include non-naturally occurring carriers, such as liposomes or other microcarriers or particles, which may act to mediate gene transfer into a recipient.

The present invention also provides for computer programs for the expression (such as visual display) of the SCF or analog three dimensional structure, and further, a computer program which expresses the identity of each constituent of an SCF molecule and the precise location within the overall structure of that constituent, down to the atomic level. Set forth below is one example of such program. There are many currently available computer programs for the expression of the three dimensional structure of a molecule. Generally, these programs provide for inputting of the coordinates for the three dimensional structure of a molecule (i.e., for example, a numerical assignment for each atom of an SCF molecule along an x, y, and z axis), means to express (such as visually display) such coordinates, means to alter such coordinates and means to express an image of a molecule having such altered coordinates. One may program crystallographic information, i.e., the coordinates of the location of the atoms of an SCF molecule in three dimensional space, wherein such coordinates have been obtained from crystallographic analysis of said SCF molecule, into such programs to generate a computer

program for the expression (such as visual display) of the SCF three dimensional structure. Also provided, therefore, is a computer program for the expression of SCF analog three dimensional structure. Preferred is the computer program Insight II, version 4, available from Biosym, San Diego, California, with the coordinates as set forth in Figure 8 input. Preferred expression means is on a Silicon Graphics 320 VGX computer, with Crystal Eyes glasses (also available from Silicon Graphics), which allows one to view the SCF molecule or its analog stereoscopically. The above-listed computer programs are only examples, and the use of such programs in the claimed methods is not limited thereto, as one of skill may use any other computer program that provides the desired three dimensional expression. Alternatively, the present SCF crystallographic coordinates and diffraction data are also deposited in the Protein Data Bank, Chemistry Department, Rutgers University, New Jersey, USA [formerly at Brookhaven National Laboratory, Upton, NY 11972]. One may use these data in preparing a different computer program for expression of the three dimensional structure of a SCF molecule or analog thereof. Therefore, another aspect of the present invention is a computer program for the expression of the three dimensional structure of a SCF molecule. Also provided is said computer program for visual display of the three dimensional structure of an SCF molecule; and further, said program having means for altering such visual display. Apparatus useful for expression of such computer program, particularly for the visual display of the computer image of said three dimensional structure of

an SCF molecule or analog thereof is also therefore here provided, as well as means for preparing said computer program and apparatus.

The computer program is useful for preparation of SCF analogs because one may select specific sites on the SCF molecule for alteration and readily ascertain the effect the alteration will have on the overall structure of the SCF molecule. Selection of said site for alteration will depend on the desired biological characteristic of the SCF analog. If one were to randomly change said SCF molecule there would be substitutions, additions or deletions, and even more analogs having multiple changes. By viewing the three dimensional structure wherein said structure is correlated with the composition of the molecule, the selection for sites for alteration is no longer a random event, but sites for alteration may be determined rationally.

Identity of the three dimensional structure of SCF, including the placement of each constituent down to the atomic level has now yielded information regarding which moieties are necessary to maintain the overall structure of the SCF molecule. One may therefore select whether to maintain the overall structure of the SCF molecule when preparing an SCF analog of the present invention, or whether (and how) to change the overall structure of the SCF molecule when preparing a SCF analog of the present invention. Optionally, once one has prepared such analog, one may test such analog for a desired characteristic.

One may, for example, seek to maintain the overall structure possessed by a non-altered natural or recombinant SCF molecule. The overall structure is presented in Figures 2A-2B, and is described in more detail below. Maintenance of the overall structure may ensure receptor binding, a necessary characteristic for an analog possessing the biologic capabilities of natural SCF (if no receptor binding, signal transduction does not result from the presence of the analog). It is contemplated that one class of SCF analogs will possess the three dimensional core structure of a natural or recombinant (non-altered) SCF molecule, yet possess different characteristics, such as an increased ability to selectively stimulate neutrophils. Another class of SCF analogs are those with a different overall structure which diminishes the ability of an SCF analog molecule to bind to a SCF receptor, Kit, and possesses a diminished ability to selectively stimulate hematopoiesis, for example, as compared to non-altered natural or recombinant SCF.

For example, it is now known which moieties within the internal regions of the SCF molecule are hydrophobic, and, correspondingly, which moieties on the external portion of the SCF molecule are hydrophilic. Without knowledge of the overall three dimensional structure, preferably to the atomic level as provided herein, one could not forecast which alterations within this hydrophobic internal area would result in a change in the overall structural conformation of the molecule. An

overall structural change could result in a functional change, such as lack of receptor binding, for example, and therefore, diminishment of biological activity as found in non-altered SCF. Another class of SCF analogs is therefore SCF analogs which possess the same hydrophobicity as (non-altered) natural or recombinant SCF. More particularly, another class of SCF analogs possesses the same hydrophobic moieties within the four helical bundle of its internal core as those hydrophobic moieties possessed by (non-altered) natural or recombinant SCF yet have a composition different from said non-altered natural or recombinant SCF.

Another example relates to external loops which are structures which connect the internal core (helices) of the SCF molecule. From the three dimensional structure -- including information regarding the spatial location of the amino acid residues -- one may forecast that certain changes in certain loops will not result in overall conformational changes.

Therefore, another class of SCF analogs provided herein is that having an altered external loop but possessing the same overall structure as (non-altered) natural or recombinant SCF. More particularly, another class of SCF analogs provided herein are those having an altered external loop, said loop being selected from the loops discussed infra. More particularly, said loops, are altered to increase the half life of the molecule by stabilizing said loops. Such stabilization may be by connecting all or a portion of said loop(s) to a portion

of an alpha helical bundle found in the core of a SCF (or analog) molecule. Such connection may be via beta sheet, salt bridge, disulfide bonds, hydrophobic interaction or other connecting means available to those skilled in the art, wherein such connecting means serves to stabilize said external loop or loops.

Additionally, such external loops may be the site(s) for chemical modification because in (non-altered) natural or recombinant SCF such loops are relatively flexible and tend not to interfere with receptor binding. Thus, there would be additional room for a chemical moiety to be directly attached (or indirectly attached via another chemical moiety which serves as a chemical connecting means). The chemical moiety may be selected from a variety of moieties available for modification of one or more function of an SCF molecule. For example, an external loop may provide sites for the addition of one or more polymer which serves to increase serum half-life, such as a polyethylene glycol molecule. Such polyethylene glycol molecule(s) may be added wherein said loop is altered to include additional lysines which have reactive side groups to which polyethylene glycol moieties are capable of attaching. Other classes of chemical moieties may also be attached to one or more external loops, including but not limited to other biologically active molecules, such as receptors, other therapeutic proteins (such as other hematopoietic factors which would engender a hybrid molecule), or cytotoxic agents (such as diphtheria toxin). This list is of course not complete; one skilled in the art possessed of

the desired chemical moiety will have the means to effect attachment of said desired moiety to the desired external loop. Therefore, another class of the present SCF analogs includes those with at least one alteration in an external loop wherein said alteration provides for the addition of a chemical moiety such as at least one polyethylene glycol molecule.

Deletions, such as deletions of sites recognized by proteins for degradation of the molecule, may also be effectual in the external loops. This provides alternative means for increasing half-life of a molecule otherwise having the SCF receptor binding and signal transduction capabilities (e.g., the ability to selectively stimulate hematopoiesis). Therefore, another class of the present SCF analogs includes those with at least one alteration in an external loop wherein said alteration decreases the turnover of said analog by proteases. One may prepare an abbreviated SCF molecule by deleting a portion of the amino acid residues found in any of the the external loops (discussed infra), said abbreviated SCF molecule may have additional advantages in preparation or in biological function.

Another example relates to the relative charges between amino acid residues which are in proximity to each other. As noted above, the SCF molecule contains a relatively tightly packed four helical bundle. Some of the faces on the helices face other helices. At the point (such as a residue) where a helix faces another helix, the two amino acid moieties which face each other may have the same

charge, and thus tend to repel each other, which lends instability to the overall molecule. This may be eliminated by changing the charge (to an opposite charge or a neutral charge) of one or both of the amino acid moieties so that there is no repelling. Therefore, another class of SCF analogs includes those SCF analogs having been altered to modify instability due to surface interactions, such as electron charge location.

The present invention provides methods for designing SCF analogs and related compositions and the products of those methods. The end products of the methods may be the SCF analogs as defined above or related compositions. For instance, the examples disclosed herein demonstrate (a) the effects of changes in the constituents (i.e., chemical moieties) of the SCF molecule on the SCF structure and (b) the effects of changes in structure on biological function.

Accordingly, therefore, the present invention provides a computer based method for preparing a stem cell factor (SCF) analog comprising the steps of: (a) providing computer expression of the three dimensional structure of of an SCF molecule using its crystal structure; (b) selecting from the computer expression of step (a) at least one site on the SCF molecule for alteration; (c) preparing an SCF molecule having an alteration at said one said selected site; and (d) optionally, testing the SCF molecule for a desired characteristic. The SCF molecule of step (a) may be naturally occurring wild type SCF or any portion or fragment thereof which is capable

of binding to SCF receptor.

In an embodiment of the above-described method the computer expression allows for display of the amino acids of the SCF molecule. In another embodiment of the method the computer expression allows for display of each atom of the SCF molecule. In a further embodiment of the method the SCF molecule is a native or a selenomethionyl SCF. In another embodiment of the method the site on the SCF molecule for alteration is a receptor binding site on the surface of the SCF molecule. In a further embodiment of the method the receptor binding site comprises amino acid residues 79-85. The SCF molecule may be a recombinant human SCF or a wild type naturally occurring human SCF. SCF wild type and recombinant may also be of other sources such as but not limited to rat or mouse. In an embodiment of the above-described method, the atomic coordinates of the crystal structure are set forth in Figure 8. In another embodiment the SCF analog comprises a polypeptide having an amino acid sequence portion of SCF capable of binding a receptor and having the overall three-dimensional conformation as shown in Figures 2A-2B, wherein the three-dimensional conformation is: a) anti-parallel, double-cross over 4-alpha helical bundle with a left hand twist; and b) overall dimensions of approximately 85 Å x 30 Å x 20 Å. In an embodiment the SCF analog comprises electron density distributions as set forth in Figures 1A, 1B, and 1C. In a further embodiment the SCF molecule is a native SCF or a selenomethionyl SCF.

In an embodiment the site on the SCF molecule for

alteration is a receptor binding site on the surface of the SCF molecule or a non-receptor site of the SCF.

Alteration of a non-receptor binding site will result in a designed SCF analog that binds to the SCF receptor but is less active such that such an analog may be used for blocking activity of the SCF.

In another embodiment the receptor binding site comprises approximately amino acid residues 79-95.

This invention provides an isolated SCF analog prepared according to the above-described method. In an embodiment the isolated SCF analog which binds to SCF receptor, Kit. In another embodiment the isolated SCF analog has an alteration in at least one atom of the atomic coordinates of the crystal structure set forth in Figure 8. In a further embodiment the SCF analog comprises a polypeptide having an amino acid sequence portion of SCF capable of binding a receptor and having the overall three-dimensional conformation as shown in Figures 2A-2B, wherein the three-dimensional conformation is: a) anti-parallel, double-cross over 4-alpha helical bundle with a left hand twist; and b) overall dimensions of approximately 85 Å x 30 Å x 20 Å. In an embodiment the SCF analog comprises electron density distributions altered from those set forth in Figures 1A, 1B, and 1C.

This invention provides a composition comprising an isolated SCF analog prepared according to the above-described method effective to treat a subject and a

pharmaceutically acceptable carrier. In an embodiment of the composition, the isolated SCF analog has an alteration in at least one atom of the atomic coordinates of the crystal structure set forth in Figure 8. In another embodiment the isolated SCF analog comprises a polypeptide having an amino acid sequence portion of SCF capable of binding a receptor and having the overall three-dimensional conformation as shown in Figures 2A-2B, or an alteration thereof, wherein the three-dimensional conformation is: a) anti-parallel, double-cross over 4-alpha helical bundle with a left hand twist; and b) overall dimensions of approximately 85 Å x 30 Å x 20 Å. In a further embodiment the isolated SCF analog comprises electron density distributions as set forth in Figures 1A, 1B, and 1C. In an embodiment the isolated SCF analog comprises a native SCF1-165, a recombinant seleno-methionyl SCF1-141, or a recombinant selenomethionyl SCF1-165.

Any of the aforementioned SCF analogs may optionally have before the first N-terminal amino acid residue a methionine at position"-1".

In an embodiment of the composition the site on the isolated SCF molecule for alteration is a receptor binding site on the surface of the SCF molecule. In a further embodiment the receptor binding site comprises approximately amino acid residues 79-95.

This invention provides a method of treating a subject having a disorder requiring SCF comprising administration

of a composition comprising an isolated SCF analog prepared by the method of preparing a SCF analog or a compound designed by the method of designing a compound capable of binding to the SCF receptor as described infra. In an embodiment the subject has a blood disorder. In another embodiment the disorder which the subject has is anemia, myeloproliferative disorder, neoplasia, nerve damage, infertility, intestinal damage, a pigmentation disorder, or immunodeficiency. In an embodiment the administration of the isolated SCF analog is for ex vivo or in vivro production of peripheral blood progenitors, ex vivo or in vivro stem cell expansion, ex vivo or in vitro growth of epithelial cells, ex vivo or in vitro growth of stromal cells, ex vivo or in vitro dendritic cell stimulation, and in vivo cell mobilization. In an embodiment the isolated SCF analog is administered orally or by any other routes described infra. In an embodiment the isolated SCF analog has an alteration in at least one atom of the atomic coordinates of the crystal structure set forth in Figure 8. In a further embodiment the isolated SCF analog comprises a native SCF1-165 or a recombinant selenomethionyl SCF1-141. In another embodiment the site on the isolated SCF molecule for alteration is a receptor binding site on the surface of the SCF molecule. In a further embodiment the receptor binding site comprises approximately amino acid residues 79-95. In an embodiment the isolated SCF analog comprises a native or recombinant SCF1-165 or a recombinant selenomethionyl SCF1-141. As used herein throughout SCF receptor is Kit.

This invention provides a method for designing a compound capable of binding to the stem cell factor (SCF) receptor site of comprising the steps of: a) determining a binding site for the SCF receptor on the SCF based on the three-dimensional structure of SCF or an SCF polypeptide or portion/fragment thereof, atomic coordinates computed from X-ray diffraction data of a crystal comprising a polypeptide having an amino acid sequence portion of SCF capable of binding the receptor; and b) designing a compound comprising an entity that binds the SCF receptor. The designed compound mimics, i.e. is a copy or simulation of the overall portion of SCF that binds to SCF receptor, Kit.

In an embodiment the design of the compound of step (b) is determined by shape complementarity or by estimated interaction energy. In another embodiment the designed compound fits an SCF receptor binding site on SCF receptor as shown in Figure 6. In a further embodiment the designed compound fits an SCF receptor binding site on SCF receptor as shown in Figures 7A or 7B. In an embodiment the designed compound has an alteration in at least one atom of the atomic coordinates of the crystal structure set forth in Figure 8. In yet another embodiment the designed compound is a double-headed SCF ligand analog having the structure set forth in Figure 10A. In a still further embodiment each ligand head of the double-headed SCF ligand analog is an oligopeptide having the structure set forth in Figure 10B. The designed compound comprises two conjugated ligands having a linker between the two ligands.

In an embodiment, the ooligopeptide comprises a sequence, wherein functional moiety F_1 corresponds to a segment of amino acid residues from within N-terminal residues 1-10 of SCF, functional moiety F_2 corresponds to a segment of amino acid residues from within residues 79-95 of SCF, and functional moiety F_3 corresponds to a segment of amino acid residues located within three amino acid residues of amino acid residue 127, wherein F_1, F_2, and F_3 are connected by connecting peptide segements X_n, X_m, and X_p, respectively, wherein n=0-5, m=0-5 and p=3-8 amino acid residues, respectively, and the conjugation moiety F_L is a cysteine residue.

A functional moiety is defined as en entity that has a particular binding property, i.e. it mimics receptor-binding sites on the surface of SCF, i.e. the ligand portion of SCF.

The amino acid residues located within 3 amino acid residues of amino acid residue 127 may be located within 3 residues in either direction of residue 127. In further embodiments the amino acid residues may be from 4 to 10 amino acid residues in either direction of amino acid residue 127.

In another embodiment of the above-described method the functional moieties F_1, F_2, and F_3 on the ligand heads have been selected by bacterial phage display for optimal receptor binding. In an embodiment the functional moieties and connecting peptide segments of an active oligopeptide ligand head are replaced by chemical

mimetics. In another embodiment an appropriate chemical scaffold of connecting segments has been designed to comprise (present) functional moieties F_1, F_2 and F_3 which have been selected by combinatorial chemistry for optimal receptor binding from a library of chemical moieties complementary to receptor-binding sites on the surface of SCF. In an embodiment the linker comprises an organic polymer having two ends capped at each end by a reactive capping moiety, F_c, which react covalently with the conjugation moiety, F_L, on the ligand head. In an embodiment the organic polymer is polyethyleneglycol (PEG) comprising the structure $H[OCH_2CH_2]_nOH$, wherein n is 10-20. In an embodiment the capping moiety, F_c, is a thiol-reactive group such as N-ethyl maleimide. In an embodiment the conjugating moiety, F_L, is a thiol containing group such as cysteine.

This invention provides a compound designed by the method of claim 32.

A composition comprising the compound designed by the above described method and a pharmaceutically acceptable carrier. In an embodiment the compound comprises an isolated SCF analog, whose alteration site is a receptor-binding site on the surface of the altered SCF molecule. In another embodiment the composition comprises a double-headed receptor SCF ligand analog having the structure set forth in Figure 10A. In an embodiment each ligand head of the double-headed SCF ligand analog is an oligopeptide having the structure set forth in Figure 10B.

In another embodiment the ooligopeptide comprises a sequence, wherein functional moiety F_1 corresponds to a segment of amino acid residues from within N-terminal residues 1-10 of SCF, functional moiety F_2 corresponds to a segment of amino acid residues from within residues 79-95 of SCF, and functional moiety F_3 corresponds to a segment of amino acid residues located within three amino acid residues of amino acid residue 127, wherein F_1, F_2, and F_3 are connected by connecting peptide segements X_n, X_m, and X_p, respectively, wherein n=0-5, m=0-5 and p=3-8 amino acid residues, respectively, and the conjugation moiety F_L is a cysteine residue. In a further embodiment the functional moieties F_1, F_2, and F_3 on the ligand heads have been selected by bacterial phage display for optimal receptor binding. In an embodiment the functional moieties and connecting peptide segments of an active oligopeptide ligand head are replaced by chemical mimetics. In another embodiment an appropriate chemical scaffold of connecting segments has been designed to comprise (present) functional moieties F_1, F_2, and F_3, which have been selected by combinatorial chemistry for optimal receptor binding from a library of chemical moieties complementary to receptor-binding sites on the surface of SCF. In another embodiment the linker comprises an organic polymer having two ends capped at each end by a reactive capping moiety, F_c, which react covalently with the conjugation moiety, F_L, on the ligand head. In a further embodiment the organic polymer is polyethyleneglycol (PEG) comprising the structure $H[OCH_2CH_2]_nOH$, wherein n is 10-20. In another embodiment the capping moiety, F_c, is a thiol-reactive group such as

N-ethyl maleimide. In an embodiment the conjugating moiety, F_L, is a thiol containing group such as cysteine.

This invention provides a method of treating a subject comprising administration of a compound designed by the above described method. In an embodiment the subject has a blood disorder. In a further embodiment the blood disorder is anemia or immunodeficiency. In an embodiment the compound is administered orally or any other routes. In an embodiment the compound is an isolated SCF analog. In another embodiment the compound comprises an isolated SCF analog, whose alteration site is a receptor binding site on the surface of the altered SCF molecule. In another embodiment of the method the composition comprises a double-headed receptor SCF ligand analog having the structure set forth in Figure 10A. In an embodiment each ligand head of the double-headed SCF ligand analog is an oligopeptide having the structure set forth in Figure 10B. In another embodiment the ooligopeptide comprises a sequence, wherein functional moiety F_1 corresponds to a segment of amino acid residues from within N-terminal residues 1-10 of SCF, functional moiety F_2 corresponds to a segment of amino acid residues from within residues 79-95 of SCF, and functional moiety F_3 corresponds to a segment of amino acid residues located within three amino acid residues of amino acid residue 127, wherein F_1, F_2, and F_3 are connected by connecting peptide segements X_n, X_m, and X_p, respectively, wherein n=0-5, m=0-5 and p=3-8 amino acid residues, respectively, and the conjugation moiety F_L is a cysteine residue. In a further embodiment the functional moieties F_1, F_2, and F_3

on the ligand heads have been selected by bacterial phage display for optimal receptor binding. In an embodiment the functional moieties and connecting peptide segments of an active oligopeptide ligand head are replaced by chemical mimetics. In another embodiment an appropriate chemical scaffold of connecting segments has been designed to comprise (present) functional moieties F_1, F_2, and F_3, which have been selected by combinatorial chemistry for optimal receptor binding from a library of chemical moieties complementary to receptor-binding sites on the surface of SCF. In another embodiment the linker comprises an organic polymer having two ends capped at each end by a reactive capping moiety, F_c, which react covalently with the conjugation moiety, F_L, on the ligand head. In a further embodiment the organic polymer is polyethyleneglycol (PEG) comprising the structure $H[OCH_2CH_2]_nOH$, wherein n is 10-20. In another embodiment the capping moiety, F_c, is a thiol-reactive group such as N-ethyl maleimide. In an embodiment the conjugating moiety, F_L, is a thiol containing group such as cysteine.

This invention provides a method of stimulating the production of hematopoietic cells in a subject comprising administering an isolated stem cell factor (SCF) analog. In an embodiment isolated stem cell factor (SCF) analog is prepared by the method of claim 1 or designed by the above described method. In another embodiment the administration is oral or any other route. In an embodiment the isolated SCF analog has an alteration in at least one atom of the atomic coordinates of the crystal structure as set forth in Figure 8. In another

embodiment the isolated SCF analog comprises amino acid residues of native or recombinant SCF1-165 or amino acid residues of a recombinant selenomethionyl SCF1-141. In an embodiment of this method the isolated SCF analog, comprises an isolated altered SCF molecule, whose alteration site is a receptor binding site on the surface of the altered SCF molecule. In another embodiment of the above-described the compound comprises an isolated SCF analog, whose alteration site is a receptor-binding site on the surface of the altered SCF molecule. In another embodiment of said method the composition comprises a double-headed receptor SCF ligand analog having the structure set forth in Figure 10A. In an embodiment each ligand head of the double-headed SCF ligand analog is an oligopeptide having the structure set forth in Figure 10B. In another embodiment the ooligopeptide comprises a sequence, wherein functional moiety F_1 corresponds to a segment of amino acid residues from within N-terminal residues 1-10 of SCF, functional moiety F_2 corresponds to a segment of amino acid residues from within residues 79-95 of SCF, and functional moiety F_3 corresponds to a segment of amino acid residues located within three amino acid residues of amino acid residue 127, wherein F_1, F_2, and F_3 are connected by connecting peptide segements X_n, X_m, and X_p, respectively, wherein n=0-5, m=0-5 and p=3-8 amino acid residues, respectively, and the conjugation moiety F_L is a cysteine residue. In a further embodiment the functional moieties F_1, F_2, and F_3 on the ligand heads have been selected by bacterial phage display for optimal receptor binding. In an embodiment the functional moieties

and connecting peptide segments of an active oligopeptide ligand head are replaced by chemical mimetics. In another embodiment an appropriate chemical scaffold of connecting segments has been designed to comprise (present) functional moieties F_1, F_2, and F_3, which have been selected by combinatorial chemistry for optimal receptor binding from a library of chemical moieties complementary to receptor-binding sites on the surface of SCF. In another embodiment the linker comprises an organic polymer having two ends capped at each end by a reactive capping moiety, F_c, which react covalently with the conjugation moiety, F_L, on the ligand head. In a further embodiment the organic polymer is polyethyleneglycol (PEG) comprising the structure $H[OCH_2CH_2]_nOH$, wherein n is 10-20. In another embodiment the capping moiety, F_c, is a thiol-reactive group such as N-ethyl maleimide. In an embodiment the conjugating moiety, F_L, is a thiol containing group such as cysteine.

This invention provides an isolated stem cell factor (SCF) molecule, which is an altered SCF, comprising any portion of amino acids 1-165 of a human SCF polypeptide, optionally comprising an N-terminal methionine before amino acid residue 1, wherein the polypeptide has an amino acid sequence portion of SCF capable of binding to the SCF receptor. In an embodiment of the altered isolated stem cell factor molecule an alteration is selected from the group consisting of deletion, insertion and substitution of at least one amino acid residue from the naturally occurring amino acid sequence of SCF.

In a further embodiment an alteration is a truncated SCF comprising amino acids 1-141 of a human SCF polypeptide, optionally comprising an N-terminal methionine before amino acid residue 1, E. In another embodiment the three-dimensional structure is altered from the atomic coordinates are set forth in Figure 8. In yet another embodiment the electron density distribution map is altered from the atomic coordinates are set forth in Figures 1A, 1B, or 1C. In a still further embodiment the substitution of at least one amino acid residue is selected from the group consisting of SCF(Y26C) disulfide-linked dimer, SCF(D25C), SCF(K62C), SCF(K78N, N81K), SCF(R117A, I118A), SCF(E92A, S95A), and SCF(D124A, K127D). In another embodiment the overall three-dimensional conformation of the stem cell factor molecule has an altered three-dimensional structure of the αC-β2 loop.

This invention provides a pharmaceutical composition comprising the above described altered isolated SCF molecule and a pharmaceutically acceptable carrier. In an embodiment the altered SCF molecule molecule is a hybrid molecule of the altered stem cell factor molecule and a second protein or fragment thereof. As used herein, an SCF hybrid molecule is defined as a molecule wherein analog SCF is combined with with part or all of another protein such as another cytokine or another protein, which for example, effects signal transduction via entry through the cell through a SCF-SCF receptor transport mechanism. In an embodiment the alteration of the αC-β2 loop is a change in length of the amino acid sequence of

the αC-β2 loop by a deletion or an insertion of at least one amino acid residue or a change in at least one amino acid residue from the naturally occurring amino acid residue(s) of the αC-β2 loop. In another embodiment the change in said at least one amino acid residue from the naturally occurring amino acid residue(s) is selected from the group consisting of SCF(Y26C) disulfide-linked dimer, SCF(D25C), SCF(K62C), SCF(K78N, N81K), SCF(R117A, I118A), SCF(E92A, S95A), and SCF(D124A, K127D).

Generally, for design of drugs as described in the above-described methods, certain changes are known to have certain structural effects. For example, deleting one cysteine could result in the unfolding of a molecule which is, in its unaltered state, is normally folded via a disulfide bridge. There are other known methods for adding, deleting or substituting amino acids in order to change the function of a protein.

The atomic coordinates may be determined in the above-described method by multiwave anomalous diffraction (MAD) measurements, but is not limited htereto, since any means determined suitable by one of skill in the art may also be used.

This invention will be better understood from the Experimental Details which follow. However, one skilled in the art will readily appreciate that the specific methods and results discussed are merely illustrative of the invention as described more fully in the claims which follow thereafter.

EXPERIMENTAL DETAILS

MATERIALS AND METHODS

SCF Expression, purification and analyses

Human SCF^{1-141} was expressed recombinantly in *E. coli* as described previously (Langley *et al.*, 1994). For expression of SeMet SCF^{1-141}, the expression vector was transfected into the methionine auxotrophic *E. coli* strain FM5. Fermentation was carried out at 30°C in 8 liters of minimal medium consisting of ammonium sulfate (10 g/liter), glucose (5 g/liter), methionine (0.125 g/liter), phosphate salts, magnesium, citric acid, trace metals, and vitamins. When an OD_{600} of 3-5 was reached, a feed medium was added that consisted of the following components in a total volume of 1 liter: 100 g of ammonium sulfate, 450 g of glucose, 2 g of methionine, magnesium, trace metals, and vitamins. At an OD_{600} of 12.4, induction medium (one liter containing 100 g of ammonium sulfate, 300 g of glucose, and 1 g of selenomethionine) was added and fermentation proceeded at 30°C. Five hours later (at an OD_{600} of approximately 16), the temperature was raised to 42°C to induce SCF expression and additional selenomethionine (1 g) was added. Cells were harvested 4 hours after the temperature shift (OD_{600} of approximately 16). SeMet SCF^{1-141} expression was estimated as 0.5 g/liter. Both SCF^{1-141} and SeMetSCF^{1-141} were purified with minor modifications to previously described procedures (Langley *et al.*, 1992, 1994). Both retain the initiating

methionine (or SeMet) residue [position (-1)] (Langley et al., 1994). N-terminal amino acid sequencing was performed as described (Lu et al., 1991). About 90% SeMet was present in SeMetSCF$^{1-141}$ at each of the Met positions, based on amino acid analysis and N-terminal sequencing results (i.e. lack of recovery of Met residues for SeMetSCF$^{1-141}$ in comparison with SCF$^{1-141}$; data not shown).

Crystallization

Crystals were obtained by the use of hanging drop vapor diffusion method under aerobic conditions. The initial crystals were grown by mixing 1 μl of protein solution [44 mg/ml for SCF$^{1-141}$ or 38 mg/ml for SeMet SCF$^{1-141}$) in 10 mM sodium phosphate pH 6.5, 80 mM NaCl] with 1 μl crystallization reservoir solution. The crystallization reservoir solution included 25% (w/w) PEG 400, 240 mM $CaCl_2$, 100 mM HEPES pH 7.4 for SCF$^{1-141}$, and 22% PEG400, 220 mM $CaCl_2$, 100 mM HEPES pH 7.2 and 5-10 mM dithiothreitol (DTT) for SeMetSCF$^{1-141}$. Crystallization trays were incubated at 20° C and crystals reached full size in approximately 3 days with typical dimensions of 0.5 x 0.2 x 0.2 mm. Microseeding and lower concentrations of DTT solution (2 mM) wre needed to reproduce SeMetSCF$^{1-141}$ crystals subsequently. An extant SeMetSCF$^{1-141}$ crystal was washed with its reservoir solution and then crushed to produce microseeds, which were stored in 50 μl of a stabilizing solution of 32% (w/w) PEG400, 260 mM $CaCl_2$, 100 mM HEPES (pH 7.4) at room temperature. For microseeding experiments, the seed stock was diluted by 10-10,000-fold with crystallization reservoir solution. A 1 μl aliquot of this prepared precipitant was mixed with 1 μl of the

protein solution to make the droplet. The crystal for MAD phasing was grown from a crystallization reservoir solution containing 2 mM DTT concentration.

Diffraction measurements

X-ray diffraction data from SCF^{1-141} crystals were recorded on two Hamlin-Xuong area detectors at 293K at a home source. The data were integrated using the UCSD software package and scaled using AGROVATA and ROTAVATA as implemented in CCP4 suite (CCP4, 1994). The MAD experiments for $SeMetSCF^{1-141}$ were conducted at the X4A synchrotron beam line of Brookhaven National Laboratory using Fuji image plates. A single crystal was frozen at 110K using paratone-N (Exxon) as a cryoprotectant. The MAD data were collected at four wavelengths (before the edge, at the SeK edge, at the peak and after the peak) in oscillations of 1.3-1.5° without overlap. The $SeMetSCF^{1-141}$ crystal was oriented such that *b*-axis was parallel to the oscillation axis and a mirror geometry was used during data collection. The MAD data were processed using DENZO and Scalepack (Otwinowski, 1993; Gewirth, 1995)(Table I).

Table I. MAD data collection and phasing statistics.

Data collection (25 - 2.0 Å)[a]

Wavelength(Å)	Unique reflections	Completeness (%)	Signal(I/ σ)	R_{sym}(%)
λ1=0.9919 (pre-edge)	65,810	95.1	18.4	6.7
λ2=0.9793 (inflection)	65,759	95.0	16.7	5.8
λ3=0.9791 (peak)	65,665	94.9	15.2	6.7
λ4=0.9686 (remote)	65,689	94.9	16.0	5.6

Anomalous diffraction ratios (20 - 2.6 Å)[b]

	λ1	λ2	λ3	λ4	f' (e)	f"(e)
λ1	0.035 (0.030)	0.051	0.042	0.035	-4.0	-0.5
λ2		0.052 (0.029)	0.033	0.051	-10.3	3.8
λ3			0.070 (0.031)	0.041	-8.1	5.6
λ4				0.055 (0.030)	-3.9	3.8

MAD phasing (25 - 2.6 Å)[c]

$R(\circ|F_T|) = 0.044$ $R(\circ|F_A|)=0.39$ $<\Delta(\Delta\Phi)> = 41.6°$ $<\sigma(\Delta\Phi)> = 18.7°$

Table I continued. MAD data collection and phasing statistics.

[a] Unique reflections are determined by point group 222 (not mmm) to distinguish Bijvoet-related reflections. Rsym = 100 x $\Sigma_{hkl}\ \Sigma_i\ |I_i - \langle I\rangle| / \Sigma_{hkl}\Sigma_i I_i$, where I_i is the ith measurement of reflection hkl and <I> is the weighted mean of all measurements of I.

[b] Anomalous diffraction ratios = $\langle \Delta|F|^2\rangle^{1/2} / \langle |F|^2\rangle^{1/2}$, where $\Delta|F|$ is the absolute value of the Bijvoet (diagonal elements) or dispersive difference (off-diagonal elements), respectively. Values in parentheses are for centric data.

[c] $R = \Sigma_{hkl}\ \Sigma_i\ |\ |F_i| - \langle F\rangle\ |\ /\ \Sigma\ |F|$. $^{o}F_T$ is the structure factor due to normal scattering from all the atoms. $^{o}F_A$ is the structure factor due to normal scattering from the anomalous scatterers only, and $\Delta\Phi$ is the phase difference between $^{o}F_T$ and $^{o}F_A$. $\Delta(\Delta\Phi)$ is the difference between two independent determinations of $\Delta\Phi$.

Molecular replacement attempts

Structure determination by the molecular replacement method was attempted for the home source data set. The MERLOT (Fitzgerald, 1988) and AmoRe (CCP4, 1994) programs were used with various four-helix bundle structures as search models, and a good rotation solution was obtained. The rotation solution agreed well with the orientation of helical bundles (approximately along the *b*-axis of unit cell) that was deduced from native Patterson maps. Dissimilarities among the helical cytokines and the multiplicity of subunits (four) hampered detection of any significant translational function peaks.

Phase evaluation

The processed MAD data were passed through the MADSYS programs (Hendrickson, 1985). Algebraic and probabilistic MAD phasing procedures (Hendrickson, 1985; Pahler *et al.*, 1990) were applied for phase determination (Table II). Selenium sites were located by HASSP program (CCP4, 1994) in F_A Patterson and difference Fourier maps and refined by MADSYS programs. The choice of enantiomer was determined by comparison of the electron density maps computed from the two enantiomorphic selenium structures to maximum Bragg spacings of 2.6 Å. The phases were improved by 4-fold non-crystallographic symmetry (NCS) averaging. The rotation-translation matrices of the NCS axes were determined by TOSS (Hendrickson, 1979) from the selenium sites and subsequently refined by LSQRHO (W.A. Hendrickson, unpublished) and RAVE (Kleywegt and Jones, 1994), and the averaging procedure by DM (CCP4, 1994).

Model building and refinement

The initial model of SeMetSCF$^{1-141}$ was built into the averaged map at 2.3 Å by using program O (Jones *et al.*, 1991). The model includes 98 core residues for each of the four molecules in an asymmetric unit. The remote wavelength after the SeK peak was used for the refinement with the Bijvoet difference applied to Se scattering factors. The *R*-value for this model, before any refinement, was 42.1% in the resolution range of 10.0 - 2.3 Å. NCS restraints were applied during the initial rounds of refinements. After several iterations of least square and simulated annealing refinement with X-PLOR (Brunger *et al.*, 1987) and manual rebuilding against SIGMAA (Read, 1986) and $2|F_o|-|F_c|$ maps, the crystallographic *R*-value is 19.9% for the current model (Table III). The sites of Ca^{2+} ions, a component of the crystallization medium, were located from a Bijvoet difference Patterson map at the remote wavelength before the SeK edge. The SCF$^{1-141}$ model was obtained by subjecting the refined SeMetSCF$^{1-141}$ model to refinement against the area-detector data set from the SCF$^{1-141}$ crystal using the XPLOR program (Brünger *et al.*, 1987). The atomic coordinates have been deposited in the Brookhaven Protein Data Bank with accession code 1scf.

Table II. Lattice and Refinement Statistics

	SeMeSCF$^{1-141}$(λ4)	Native
Lattice		
Space group	$P2_12_12_1$	$P2_12_12_1$
Cell constants (a,b,c)(Å)	71.8, 82.6, 88.2	73.0, 84.7, 88.8
Z_a[a]	4	4
Refinement[b]		
Resolution range (Å)	20.0 - 2.2	8.0 - 3.3
Completeness (%)	96.6	98.6
Unique reflections[c]	49851	7990
R-value[d] ($\|F\|>2\sigma$)(%)	19.9	20.8
R_{free}[e] (%)	24.2	27.3
R_{sym}[f] (%)	5.6	15.2
Model parameter		
Total non-H atoms	3804	3502
Total residues	448	447
Total water molecules	264	0
Total metal ions	3	0
rms bond length/angle	0.016/2.5°	0.017 / 3.0°
Average *B*-factor (Å^2)	32.1	18.7
main-chain rms *B* (bond, angle) (Å^2)	1.2/1.6	1.9/2.2
side-chain rms *B* (bond, angle) (Å^2)	2.1/2.4	3.0/3.3

[a] Z_a: number of molecules in the asymmetric unit.

[b] The reflection data higher that the resolution range were not included in the refinement due to poor R_{sym} in these resolution shells.

[c] Unique reflections are determined by point group 222 for the SeMetSCF$^{1-141}$ dataset to distinguish Bijvoet-related reflections and by point group mmm for native dataset.

[d] R-value = $\Sigma_{hkl}||F_o|-|F_c||/\Sigma_{hkl}|F_o|$.

Table II. continued Lattice and Refinement Statistics

[e]A subset of the data (6%) was excluded from the refinement and used for the free *R*-value calculation.
[f] R_{sym} for $SeMetSCF^{1-141}$ data set was calculated in the resolution range of 25-2.2 Å and for the SCF^{1-141} data set in the resolution range of 13-3.3 Å.

Structure analysis

Solvent accessibilities were defined as compared with the corresponding Gly-X-Gly peptide (Shrake and Rupley, 1973) as calculated by XPLOR (Brunger *et al.*, 1987). Structural superimpositions were performed based on a-carbon atoms alone. The coordinates were taken from the Brookhaven Data Bank with entry codes: M-CSF, 1hmc (Pandit *et al.*, 1992); IL-4, 1rcb (Wlodawer *et al.*, 1992); GM-CSF, 1gmf (Diederichs *et al.*, 1991) IL-2, 3ink (McKay, 1992); IL-5, 1hul (Milburn *et al.*, 1993). Initial segments of equivalence between two structures were defined according to equivalent secondary structure elements. These structures were then superimposed using program TOSS (Hendrickson, 1979) and the number of equivalent atoms were extended using Lsq_imp command in program O (Jones *et al.*, 1991). A cutoff distance of 3.0 Å and at least three residues in a consecutive fragment were used as the criteria of defining equivalent atom sets. Different initial equivalent segments did give different results in the structural alignment, as Rozwarski *et al* observed in their study (Rozwarski *et al.*, 1994). In this study, several initial sets of equivalent segments for each alignment were tried and the one that generated in the greatest number of equivalent atoms after the Lsq_imp extension was retained.

RESULTS AND DISCUSSION

Structure determination

Both native and selenomethionyl (SeMet) human SCF^{1-141} were expressed as recombinant proteins in *E. coli* (Langley *et al.*, 1994). Crystals grew in space group $P2_12_12_1$ with four SCF subunits and 39% solvent in the asymmetric unit. The attempts to solve the crystal structure of SCF^{1-141} by molecular replacement from other cytokine models gave good rotation solutions, but no significant translation function peaks. Experimental phases for $SeMetSCF^{1-141}$ were then evaluated in a multiwavelength anomalous diffraction (MAD) experiment. Four-wavelength data were measured from a single, frozen $SeMetSCF^{1-141}$ crystal and analyzed with MADSYS (Hendrickson, 1985). Twelve selenium sites were found in four congruent sets that proved to be associated with the respective SCF subunits in the crystal. A MAD-phased electron-density map was calculated at 2.3Å resolution (**Figure 1A**) and improved by molecular averaging (**Figure 1B**) and refinement (**Figure 1C**).

An atomic model was fitted to the experimental maps and refined at 2.2Å resolution to an *R*-value of 0.199 ($|F| > 2\sigma$) with stereochemical ideality typified by the r.m.s. deviation from bond ideality of 0.016Å. There are no residues in energetically disfavored regions of the Ramachandran plot. This model for $SeMetSCF^{1-141}$ has 3804 non-hydrogen atoms from 448 amino acid residues, 264 water molecules, three Ca^{+} ions and one polyethylene glycol (PEG) moiety. All four polypeptide chains

(designated A, B, C, and D) are sufficiently disordered before residue 11 to preclude modeling of this portion, and none of them is fully ordered through to the end. Specifically, A92-103, B130-136, B139-141, C92-103, C127-141, and D91-103 and D128-141 are all disordered. This disorder is such that, of the eight disulfide bridges, only two are seen. To test whether the reducing agent used to crystallize SeMetSCF$^{1-141}$ (see Materials and Methods) might have broken these bonds and caused the disorder, the native SCF$^{1-141}$ structure which was crystallized without reducing agent was also refined. The two crystals are nearly isomorphous (differences are due to temperature at data collection), and the two structures show the same pattern of order-disorder.

Structure of SCF

The four independent SCF subunits in the crystal are similar but distinctive, and identification of the AB and CD pairs as the molecular dimers is unmistakable. None of the SCF monomer copies is complete, but each flexible portion except for the N-terminus is stabilized by lattice contacts to another monomer. Thus, through the combination of chains A and B there are images for all but residues 1-10, and the position of Cys89 to which Cys 4 must bridge, determines the approximate course of this disordered segment. The overall structure of this composite SCF dimer is shown in **Figure 2A** and the C_α backbone for the actual AB dimer is drawn in stereo in **Figure 2B**. Topologically, SCF structure is similar to other short-chain helical cytokines (Rozwarski *et al.*,

1994) with a core of four helices (αA, αB, αC and αD) and two beta strands, β1 between αA and αB and β2 between αC and αD. Apart from the tight β2-αD connection, however, the segments outside these core elements are unique in conformation if not in length. In particular, there is an additional one-turn helix, αB', between β1 and αB, there is an exceptional hairpin loop between αB and αC at the dimer interface, and there is another extra one-turn helix, αD', in the C-terminal extension. The bounds of secondary-structure elements are given in **Figure 3**.

The core SCF dimer has its subunits arranged in a head-to-head manner with the opposed four-helix bundle axes nearly coincident (**Figure 2**). This gives the molecule an elongated shape, ~ 85Å x 30Å x 20Å. Approximately 855 Å² of surface area is buried from each protomer into the dimer interface. The interface is dominated by contacts from the C-terminal end of αA and the αA-β1 connection of one monomer to the αB-αC loop of the other monomer (**Figure 2**), and the reciprocal pair is related by an approximate dyad axis of symmetry. The actual symmetry operators have rotational and translational components of 176.3° and 0.33°, respectively, for the AB dimer and 177.4° and 0.04° Å for the CD dimer. The two dimers thereby deviate significantly and similarly (with A matched to C and B matched to D) from true 2-fold symmetry. Nevertheless, since interatomic contacts at the interface are symmetric, it is presumed that thses deviations reflect flexibility rather than inherent asymmetry.

Then the r.m.s. deviation for the C_α positions in common between the two dimers is 0.80 Å (208 C_α atoms) is comparable to that of pairwise comparisons among the four independent molecules (from 0.57 Å to 0.94 Å for 103 C_α atoms). If D alone is superimposed onto B, a rotation of 2.1° brings A and C into optimal superposition. In the contrary match-up, with D onto A, a rotation of 6.7° is needed to superimpose B and C.

The crystal structure is compatible with solution biochemistry. Consistent with the relative rates of in vitro oxidation of methionyl residues (Hsu et al. 1996), Met36 and Met48 are buried in the hydrophobic core whereas Met27 is solvent accessible. Furthermore, as predicted on the basis of fluorescence spectroscopy studies (Arakawa et al., 1991), Trp41 is buried within the hydrophobic core.

Natural SCF and Chinese hamster ovary(CHO) cell-expressed recombinant SCF are heavily glycosylated by both N-linked and O-linked carbohydrates. All four potential N-linked sites are in the SCF^{1-165} are in the SCF^{1-141} portion that has been crystallized (Langley et al., 1992; Lu *et al.*, 1992). Although the recombinant proteins expressed in bacteria are non-glycosylated, both human and rat SCF expressed in *E. coli* and then refolded *in vitro* have native structures, as judged by biophysical methods and *in vitro* biopotency assays (Arakawa et al., 1991; Langley et al., 1992) . The crystal structure of the recombinant SCF in this study is compatible with the glycosylation pattern found for SCF expressed from mammalian cells.

Thus, the potential site at Asn72, which is unglycosylated in both human and rat natural SCF expressed from mammaliam cells, is buried in the dimer interface, whereas the site at Asn120, which is fully glycosylated in both species, is accessible in the atomic model. Other sites (Asn65 in both human and rat, human Asn93 and rat Asn109) are glycosylated in some molecules but not others. These sites are also accessible in the atomic model. Asn93 is located in the highly flexible region between αC and β2, and its side chain is disordered.

Although natural SCF is a noncovalently associated dimer, recombinant human SCF produced in *E. coli* can fold alternatively *in vitro* into a covalently-linked dimer. These dimers have Cys4-Cys89' and Cys43-Cys138' intermolecular disulfide bonds (Lu *et al.*, 1996). The disulfide-linked and natural non-covalently associated SCF dimers are similar with regard to biochemical and biophysical properties, biopotency and receptor-binding affinity. The disulfide-linked SCF is also biologically active with higher biopotency in supporting growth of hematopoietic cell line and stimulating hematopoietic cell colony formation but slightly lower binding affinity to c-Kit than the noncovalently associated dimer. It was proposed that the disulfide-linked dimer arises from a double-swap of αA and αD helices between the monomers (Lu *et al.*, 1996). The crystal structure of SCF, however, suggests that a single-swap at the αB-αC loop near residue 68 is more likely.

Comparison with other short-chain helical cytokines

Although SCF has the characteristic features of short-chain helical cytokines, as among other members, both sequence and structure are highly divergent. If anything, SCF resembles the others less than they resemble one another (**Table III**). The comparison in this study of SCF with other short-chain helical cytokine structures [granulocyte-macrophage colony-stimulsting fasctor (GM-CSF) (Diederichs et al., 1991), , M-CSF (Pandit e al., 1992), interleukin (IL)-2 (McKay, 1992), IL-4 (Wlodaver et al., 1992) , and IL-5 (Milburn et al., 1993)] shows greatest structural similarity with M-CSF or IL-4, but even here fewer than half of the residues can be superimposed (**Table III**). Sequence similarities are essentially random. A structure-based sequence alignment (**Figure 3**) of SCF with other short-chain helical cytokines has pairwise identities ranging from 6.7% to 18.8% (**Table III**) and not even a single residue in SCF is conserved in all the others. Moreover, the best alignment presented in Figure 3 is only valid for the specified criteria herein, and it differs somewhat from that given by Rozwarski et al. (Rozwarski *et al.*, 1994). Indeed, because of variability in the core structures in this divergent superfamily, a self-consistent pairwise alignment of the family members has not been able to be achieved. Nevertheless, the core elements are remarkably similar in structure.

Table III. Structural and sequence comparisons of short-chain helical cytokines.

	SCF	M-CSF	IL-4	GM-CSF	IL-2	IL-5
SCF		14.1 (13.0)	12.7 (12.3)	12.5 (23.5)	18.8 (16.4)	6.7 (21.1)
M-CSF	64 (1.755)		14.8 (18.9)	13.8 (18.3)	17.5 (17.1)	10.5 (18.6)
Il-4	63 (1.578)	54 (1.820)		26.6 (25.0)	14.5 (22.2)	18.9 (18.9)
GM-CSF	48 (1.632)	58 (1.814)	64 (1.559)		9.8 (26.0)	20.4 (14.7)
IL-2	48 (1.700)	57 (1.581)	69 (1.330)	61 (1.482)		14.5 (22.2)
IL-5	45 (1.695)	38 (1.721)	53 (1.324)	49 (1.334)	62 (1.371)	

Structural comparisons and sequence comparisons between the short-chain helical cytokines are given in the lower and upper triangles, respectively. Structural comparisons are given as the maximum number of equivalent α-carbon atoms between two short-chain helical cytokines, and the r.m.s. deviation (Å), (in parentheses). Sequence comparisons are given as the percentage of sequence identity from sequence alignment based on structural superimposition, and that based on the sequence alignment from BESTFIT program of the GCG package (in

Table III. continued Structural and sequence comparisons of short-chain helical cytokines.

parentheses). The latter alignment is based only on maximizing the percentage of identity, similarities and length of the matching sequences, and the sequences submitted to the BESTFIT program were restricted within the region as defined in the PDB files, including the disordered residues. With the advantage of the relatively large number of independent data points (15 pairs), the correlation between sequence similarity and structural deviation was analyzed. Without any restriction of structural alignment, the correlation coefficient (*C*) between structural deviation and sequence identity is -0.21 and the student's *t* probability (*P*) is 0.44, suggesting little correlation between a specific sequence and the tertiary fold. With the restriction of structural alignment, however, *C* is-0.30 and *P* 0.28, indicating that the structure-based sequence identity and structural deviation are weakly connected (as also observed in another highly diverged protein family, hemoglobin; Aronson *et al*., 1994).

Core portions aside, SCF differs markedly from other short-chain helical cytokines, as indeed they differ from one another (Figure 3; Rozwarski *et al.*, 1994)). First, helix αA of SCF is unusually shortened at its N-terminus. Its disordered extension must deviate toward αC, as in M-CSF but not in the others, by virtue of the Cys4-Cys89' disulfide bridge in common with M-CSF. Secondly, the conformation of the αA-β1 connection is distinctive as required for the dimer interface, and the β1-αB connection uniquely has αB'. Again at the dimer interface, the αB-αC loop extends out distinctively along the dyad axis. Thirdly, the unusually long αC-β2 loop of SCF is both highly flexible (only one ordered copy) and with a path of its own when ordered. Finally, the C-terminal extension after αD compares only to that of M-CSF, and then only in its general direction of exit out past αB and the β- strands.

Among the short-chain helical cytokines, SCF is most closely related to M-CSF. These two have similarities in gene structure, alternative splicing, proteolytic maturation, disulfide bridging, dimer assembly, and receptor type (these similarities also extend to the Flt-3igand; Lyman and Jacobsen, 1998). Despite negligible sequence identity, an alignment and secondary structure prediction prompted by these relationships (Bazan, 1991) fits the actual

structure amazingly well, except for shifts in αB and in the αC-β2 loop. Here reality confounds logic; unexpectedly, comparable glycosylation sites (Asn120 in SCF and Asn122 in M-CSF) are displaced by one helical turn and comparable disulfide bridges (Cys43-Cys138' in SCF and Cys48-Cys139' in M-CSF) are not superimposible structurally (**Figure 4**).

Both were roughly correct in secondary-structure prediction for helices αA and αC, but substantial misplacements were made for helices αB and αD and strand β2. In the study of Rozwarski et al. (Rozwarski *et al.*, 1994), the alignment for αB is incorrect by a shift of 14 residues and that for β2 and αD by a shift of 7 residues. Bazan's earlier sequence alignment (Bazan, 1991) fits to the structural alignment herein amazingly well, except for a shift of one residue for αB and a three-residue gap in the αC-β2 loop.

Comparison with other cytokine dimers

Helical cytokines dimerize in various ways (Sprang and Bazan, 1993). Among the five dimeric helical cytokines for which crystal structures have been described [M-CSF, IL-5, ciliary neurotrophic factor (CNTF), interferon-γ (IFN-γ) and IL-10], only IFN-γ and IL-10 are similar dimers. These latter two have a 'tip-to-tip' packing with helix axes approximately perpendicular. Otherwise, the only salient

feature in common is having the subunits oriented with bundle axes aligned in parallel and helix dipoles positioned to compensate. There is 'head-to-head' packing of the four-helix bundles in M-CSF, 'tail-to-tail' packing in IL-5, and 'side-to-side' packing in CNTF. Moreover, IFN-γ, IL-10 and IL-5 are all interdigitated dimers with helices swapped between subunits. Thus, although SCF relates most closely to M-CSF, the dimer structure could not be deduced readily beforehand.

SCF in keeping with its relationship to M-CSF, is a non-interdigitated 'head-to-head' dimer (**Figure 4**). The two interfaces between promoters are completely different, however. One αA-β1 loop of M-CSF is situated between the αA-β1 and αB-αC loops of the other protomer, whereas in SCF each αA-β1 loop interacts only with αB-αC loop of the partner. This staggered mode of M-CSF dimerization (**Figure 4B**) is dictated by the position of the Cys31-Cys31' intermolecular disulfide bond in M-CSF. The dyad axes are similarly oriented in the two cases (perpendicular to the bundle axis and parallel to the αA-αD and αB-αC helix planes), but whereas the dyad axis in SCF nearly intersects the bundle axis, that in M-CSF is offset toward the αA-αD helix pair (Figure 4). Thus, when one protomer of an SCF dimer is superimposed onto one from M-CSF, the superimposition of the two mates requires a translation of 3.8 Å but a rotation of only 4.7°.

Location of the binding site for the receptor Kit

SCF binds with high affinity (nM range) to its receptor (Philo *et al.*, 1996; Broudy, 1997)). Various structure-function studies and analyses help to define residues of SCF that may be involved in this binding. These studies include mutagenesis experiments, immunochemical mapping, comparative analyses of inter-species ligand-receptor interactions, and analyses of glycosylation. Residues thereby implicated in receptor binding can then be mapped onto the surface of SCF as defined by the crystal structure. Although a precise definition of the receptor-binding site on SCF will require direct structural information on the complex of SCF with the Kit receptor, this mapping of the binding site provides a crude picture that is useful when coupled with information on Kit and related receptors.

From studies of truncation and point mutants, Langley *et al* (1994) demonstrated that the N-terminal residues 1-4 and 1-10 and the Cys4-Cys89 disulfide bond are required for receptor binding and bioactivity, and that the Cys43-Cys138 disulfide bond and C-terminal residues past 127 are not required for receptor binding but may have some roles in cell proliferation activity. Moreover, alterations at Asn10 and Asn11 brought about by chemical isomerization or by mutagenesis have positive or negative effects depending on the substitution (Hsu *et al.*, 1998). A quadruple

mutant of SCF (Arg121Asn, Asp124Asn, Lys127Asp and Asp128Lys) was found to be defective in bioactivity (Matous *et al.*, 1996). The molecular cause of this deficiency may be specific to Lys127 or due to indirect electrostatic effects. Arg121 and Asp124 are adjacent to the main N-linked glycosylation site, which is not involved in binding (see infra), and Asp128 is absent in the 1-127 truncation mutant that retains full receptor-binding activity (Langley *et al.*, 1994). Moreover, a study of human-murine SCF chimeras narrowed the important receptor recognition epitopes to within residues 1 to 35 and 79 to 97 (Matous *et al.*, 1996), and the epitope of a neutralizing antibody was mapped to the region of residues 60-95 (Mendiaz et al., 1996) and 79-97 (Matous et al., 1996).

Although SCF molecules from different mammalian species are very similar (>75% identity), there are substantial differences in inter-species receptor activation. Human SCF activates murine Kit very poorly, rodent SCF has only slightly lower potency than human SCF in binding/activating human Kit (Martin *et al.*, 1990; Lev *et al.*, 1992), and canine SCF activates human Kit slightly better than human SCF does itself (K.E. Lang, unpublished data). It is likely that the receptor-binding regions involve residues that are different between man and mouse but conserved between man and dog. These residues can be classified into five groups in the sequence (**Figure 5**). Most residues in group III are buried

and those in group II are close to the dimer interface. The residues in groups III (45-58) are buried and those in group II (24-34) are close to the dimer interface. The results in groups I (1-15), IV (80-117) and and V (130-140) are more likely to be involved in direct receptor binding.

The heavy glycosylation of natural and CHO cell-derived recombinant SCFs sheds light on the question whether residues in vicinity of αD, the equivalent of the major receptor binding site in GH, are involved in receptor binding. Human SCF expressed in CHO cells is approximately 30% by weight (Arakawa *et al.*, 1991) The main glycosylation site is at Asn120 (Langley et al., 1992). Glycosylation at this site, which is near the center of the αD helix, does not appear to influence biological activity; therefore, the area around this residue cannot be involved in receptor binding. Glycosylation of human SCF at either Asn65 or Asn93 lowers the biological activity approximately 10-fold; therefore, these residues may be near but not directly at the binding site.

Taken together, these observations indicate that the receptor-binding site may include residues from the first few N-terminal residues, the 79-95 region (mainly located on αC helix) and the C-terminal end of αD (around 127). These regions are contiguous on the SCF surface in the atomic model provided herein. The putative receptor-binding site of M-CSF

was mapped to a similar region (Taylor *et al.*, 1994).

Structural characteristics of SCF-Kit and related ligand-receptor complexes

Kit, the receptor for SCF, is a class III receptor tyrosine kinase. This class, which includes the receptors for PDGF and M-CSF, is also closely related to the class IV receptors for FGF and the class V receptors for VEGF, Flt-3 ligand and KDR (Fantl *et al.*, 1993). The ligand-binding portions of these receptors are all composed of immunoglobulin(Ig)-like domains and the kinase domains all include kinase insert sequences. The three classes are distinguished by the number of Ig repeats (five for class III, three for class IV and seven for class V) and by the length of kinase insert, which corresponds to an excursion between two helices of the kinase structure. These Ig-like receptors share similar signal transduction pathways, chromosomal localization and gene organization (Rousset *et al.*, 1995), but their ligands come with completely unrelated topologies as typified by VEGF (cystine knot) on the one hand, versus M-CSF, SCF and Flt-3 ligand (helical cytokine) on the other. Even receptors of the same class have unrelated ligands; thus both SCF and PDGF use class III receptors and VEGF anf Flt-3 ligand use class V receptors. The amino acid sequences of the ligands are extremely dissimilar

even when the fold is the same, as for PDGF vs. VEGF (25% identity) and M-CSF vs SCF (14% identity).

Although Ig-like receptors have very similar kinase portions (70% amino acid sequence identity between III and V) and about 50% identity for III or V with IV) their Ig-like domains are dissimilar in sequence both between repeats within a molecule and also at comparable positions between different receptors. (Rousset et al., 1995) Nevertheless, there are features of the receptor-ligand interaction that the class III and class V receptors have in common. First, for every studied example, the ligand binding function has been localized to the first three Ig-like domains and, where defined, to domains D2 and D3 specifically (Heidaran *et al.*, 1990; Blechman *et al.*, 1993; Lev *et al.*, 1993; Wang *et al.*, 1993; Davis-Symyth *et al.*, 1996; Barleon et al., 1997). Secondly, the ligands for all of these receptors are functional as dimers; M-CSF, VEGF and PDGF are covalently dimers, while SCF and Flt-3 ligand are non-covalently linked dimers. In each case, signaling occurs through ligand-mediated receptor oligomerization (Heldin, 1995). For SCF-Kit, it has been shown directly by biophysical methods that complexes containing toe SCF subunits and two Kit extracellular domain molecules can form in solution (Philo et al., 1996). The genetic organization of these receptor genes has the placements and phases

of introns in common (Agnes *et al.*, 1997) and the extracellular domains can be recognized from sequence motifs as telokin-like, I-set members of the Ig superfamily (Bateman and Chothia, 1995; Harpaz and Chothia, 1994).

The structure of domain D2 of Flt-1 receptor in complex with VEGF (Wiesmann *et al.*, 1997) provides a template for ligand interactions with PDGF-related receptors. Wiesmann *et al.* (1997) modeled the interaction of VEGF with D1D2D3D4(Flt-1) and discussed the likelihood that other ligand complexes with class III and class V receptors may be similar. In lightof the structure of SCF and the identified location of receptor-binding sites, the SCF-Kit complex is modeled herein.

The D2(Flt-1) domain is similar in structure to telokin, as predicted (Harpaz and Chothia, 1994), and thereby also to both domains in the structure of vascular cell adhesion molecule (VCAM)-1 (Jones *et al.*, 1995). To test the validity of VCAM-1 as a model for D2D3(Flt-1) and D2D3 (Kit), used herein was a prediction-based threading program (Fisher and Eisenberg, 1996) to thread the sequences of the Ig-like domains of Flt-1 and Kit into the telokin and VCAM-1 structures. Fits were achieved with moderate to very high confidence of similarity. The resulting structure-based sequence alignment of D2D3(Kit) with the VCAM-1 template (five gaps) has a continuous domain boundary, and residues Cys151

and Cys183 in D2(Kit) are positioned properly to make an additional disulfide bridge between strands C and F.

Characteristics of the SCF-Kit interaction

Although it has been suggested (Matous *et al.*, 1996; Mendiaz *et al.*, 1996) that SCF may interact with its receptor in a manner analogous to the ligand-receptor interactions of another helical cytokine, growth hormone (de Vos *et al.*, 1992), an alternative mode of interaction can be contemplated given the similarities among Ig-like tyrosine-kinase receptors described above. If these similarities extend to the signaling interaction, the structure of the complex of VEGF with domain D2 of Flt-1 (Wiesmann *et al.*, 1997) should provide a template for the interaction despite the disparate structures of the ligands.

To test this hypothesis next constructed was a model of the VEGF-D2D3(Flt-1) receptor complex from a rigid-body superposition of VEGF (Muller *et al.*, 1997) and VCAM-1 such as to mimic the reported VEGF- D2(Flt-1) structure (Wiesmann *et al.*, 1997). Then, keeping the dyad-symmetric receptor pair fixed, VEGF was successively replaced with the other Ig-like receptors ligands of known three-dimensional structure: PDGF (Oefner *et al.*, 1992), M-CSF (Pandit *et al.*, 1992), and SCF (this work). Each was placed on the dyad axis and

positioned to optimize contacts between the VEGF-binding site on the receptor and the putative receptor-binding regions of the ligands. Remarkably, these disparate dimeric ligands have similar spacings between binding sites and a satisfactory fit is possible for each (Figure 6). Also constructed were simple homology models of the various receptors with changes in the backbone only to accommodate insertions and deletions. The model for SCF with D2D3(Kit) shows a striking electrostatic complementarity between a highly negative binding surface on SCF and a positive surface on Kit (**Figures 7A and 7B**). The glycosylation sites on both molecules are also compatible with unimpeded interaction.

The Kit receptor is activated by both soluble and membrane-bound forms of SCF, and signaling from the membrane-bound form appears to be have *in vivo* roles (se Lyman and Jacobsen, 1998). Moreover, as in the case of Flt-1 (Barleon et al., 1997), the D4(Kit) may be involved in inter-receptor contacts in the signaling dimer (Blechman *et al.*, 1995) [although this proposal for Kit has been questioned (Philo *et al.*, 1996; Lemmon et al., 1997)]. The model constructed herein for the SCF-Kit complex is compatible with these properties (**Figure 7A and 7B**). The C-termini of the SCF dimer are directed oppositely from those of Kit, as would be appropriate for a cell-cell contact, and the receptor units cross naturally at D4. It is

noteworthy that the ligands of other Ig-like receptors also have membrane-bound forms (M-CSF and Flt-3 ligand) or are typically complexed to the extracellular matrix (Kawasaki and Ladner, 1990; Lyman and Jacobsen, 1998).

The ligand-receptor structures that are suggested herein for the Ig-like kinase receptors are remarkable. Despite marked differences in ligand structure as typified by VEGF(cystine knot), SCF (helical cytokine) and FGF (beta trefoil), the geometrical configurations of receptor binding sites on these ligands are alike. Coupled with features in common among the receptors and in their biology, a similar mode of ligand-receptor interaction across the Ig-like subfamily of receptor tyrosine kinases seems plausible.

SECOND SERIES OF EXPERIMENTS

Based on the X-ray crystallographic structure of SCF, several analogs were made and their biological activities were measured and compared to that of SCF wild type.

Analogs	Biological Activity (Approximate, compared to wild type SCF)
SCF(Y26C) disulfide linker	2 to 3 fold higher
SCF(D25C)	100 fold lower
SCF(K62C)	7 fold lower

These analogs were designed based on the structure of the dimer interface of SCF, which is a non-covalent dimer. Leu22, Pro23, Lys24, Asp25, Tyr26, Lys62 and Phe63 are in the dimer surface. The side chains of Leu22, Pro23, Tyr26, and Phe63 reside in the buried center of the dimerization site and are involved in hydrophobic interactions. The hydrophilic side chains of Lys24, Asp25 and Lys62 from each monomer residue in the solvent accessible surface, and are involved in ionic interactions. By replacing Tyr26 with Cys, [SCF(Y26C)], it was anticipated that a dimer covalently linked by a disulfide bond between the C26 residue of each monomer would form because the distance between the β carbons of the two Cys26 rresidues would be less than 3Å.

Analogs	Biological Activity (Approximate, compared to wild type SCF)
SCF(K78N, N81K)	3 fold lower
SCF(R117A, I118A)	10 fold lower
SCF(E92A, S95A)	no change
SCF(D124A, K127D)	no change

These analogs were designed based on the assumption that there may be two distinct receptor binding sites, per monomer, as with growth hormone. One site would be on the face between helix A and helix C, and the other site would be on the face between helix A and helix D.

References

Agnes, F., et al. (1997) Genomic organization of the extracellular coding region of the human FGFR4 and FLT4 genes: Evolution of the genes encoding receptor tyrosine kinases with immunoglobulin-like domains. *J. Mol. Evol.*, **45**, 45-49.

Anderson, D. M., et al. (1990) Molecular cloning of mast cell growth factor, a hematopoietin that is active in both membrane bound and soluble forms. *Cell*, **63**, 235-243.

Andre, C., et al. (1992) Genomic organization of the human c-kit gene: Evolution of the receptor tyrosine kinase subclass III. *Oncogene*, **7**, 685-691.

Arakawa, T., et al. (1992) Molecular weights of glycosylated and nonglycosylated forms of recombinant human stem cell factor determined by low-angle laser scattering. *Analytical Biochem.*, **203**, 52-57.

Arakawa, T., et al. (1991) Glycosylated and unglycosylated recombinant-derived human stem cell factor are dimeric and have extensive regular secondary structure. *J. Biol. Chem.*, **266**, 18942-18948.

Aronson, H.-E. G., et al. (1994) Quantification of tertiary structural conservation despite primary

sequence drift in the globin fold. *Prot. Sci.*, **3**, 1706-1711.

Barleon, B., et al. (1997) Mapping of the sites for ligand binding and receptor dimerization at the extracellular domain of the vascular endothelial growth factor receptor flt-1. *J. Biol. Chem.*, **272**, 10382-10388.

Bateman, A. and Chothia, C. (1995) Outline structures for the extracellular domains of the fibroblast growth factor receptors. *Nature Structural Biology*, **2**, 1068-1074.

Bazan, J. F. (1991) Genetic and structural homology of stem cell factor and macrophage colony-stimulating factor. *Cell*, **65**, 9-10.

Bella, J., et al. (1998) The structure of the two amino-terminal domains of human ICAM-1 suggests how it functions as a rhinovirus receptor and as an LFA-1 integrin ligand. *Proc. Natl. Acad. Sci. USA*, **95**, 4140-4145.

Besmer, P. (1997) Kit-ligand-stem cell factor. In Garland, J.M., Quesenberry, P.J. and Hilton, D.J. (eds), Colony-Stimulating Factors: Molecular and Cellular Biology, 2nd edn., Marcel Dekker, Inc., New York, NY, PP. 369-404.

Blechman, J. M., et al. (1993) Soluble c-kit

proteins and antireceptor monoclonal antibodies confine the binding site of the stem cell factor. *J. Biol. Chem.*, **268**, 4399-4406.

Blechman, J. M., et al. (1995) The fourth immunoglobulin domain of the stem cell factor receptor couples ligand binding to signal transduction. *Cell*, **80**, 103-113.

Broudy, V. C. (1997) Stem cell factor and hematopoiesis. *Blood*, **90**, 1345-1364.

Brünger, A. T., et al. (1987) Crystallographic *R*-factor refinement by molecular dynamics. *Science*, **235**, 458-460.

Casasnovas, J. M., et al. (1997) Crystal structure of ICAM-2 reveals a distinctive integrin recognition surface. *Nature*, **387**, 312-315.

Casasnovas, J. M., et al. (1998) A dimeric crystal structure for the N-terminal two domains of intercellular adhesion molecule-1. *Proc. Natl. Acad. Sci. USA*, **95**, 4134-4139.

Collaborative Computational Project Number 4 (1994) The CCP4 suite: programs for protein crystallography. *Acta Crystallogr.*, D, **50**, 252-270.

Davis-Symyth, T., et al. (1996) The second immunoglubulin-like domain of the VEGF tyrosine

kinase receptor Flt-1 determines ligand binding and may initiate a signal transduction cascade. *EMBO J.*, **15**, 4919-4927.

de Vos, A. M., et al. (1992) Human growth hormone and extracellular domain of its receptor: crystal structure of the complex. *Science*, **255**, 306-312.

Diederichs, K., et al. (1991) Novel fold and putative receptor binding site of granulocyte-macrophage colony-stimulating factor. *Science*, **254**, 1779-1782.

DiGabriele, A. D., et al. (1998) Structure of a heparin-linked biologically active dimer of fibroblast growth factor. *Nature*, **393**, 812-817.

DiMario, J., et al. (1989) Fibroblast growth factor in the extracellular matrix of dystrophic (mdx) mouse muscle. *Science*, **244**, 688-690.

Ealick, S. E., et al. (1991) Three-dimensional structure of recombinant human interferon-gamma. *Science*, **252**, 698-702.

Evans, S. V. (1993) SETOR: Hardware lighted three dimensional solid model representations of macromolecules. *J. Mol. Graphics*, **11**, 134-138.

Fantl, W. J., et al. (1993) Signalling by receptor tyrosine kinases. *Annu. Rev. Biochem.*, **62**, 453-481.

Fenstermaker et al., (1993) A cationic region of the platelet-derived growth factor (PDGF) A-chain (Arg159-Lys160nLys161) is required for receptor binding and mitogenic activity of the PDGF-AA homodimer., *J. Biol. Chem.*, **268**, 10482-10489.

Fisher, D. and Eisenberg, D. (1996) Fold recognition using sequence-derived predictions. *Prot. Sci.*, **5**, 947-955.

Fitzgerald, P. M. D. (1988) MERLOT, an integrated package of computer programs for the determination of crystal structures by molecular replacement. *J. Appl. Crystallogr.*, **21**, 273-278.

Flanagan, J. G. and Leder, P. (1990) The kit ligand: a cell surface molecule altered in steel mutant fibroblasts. *Cell*, **63**, 185-194.

Fukuda, N., et al. (1997) Role of long-form PDGF A-chain in the growth of vascular smooth muscle cells from spontaneously hypertensive rats. *Am. J. Hypertens.*, **10(10 Pt 1)**, 1117-1124.

Galli, S. J., et al. (1994) The kit ligand, stem cell factor. *Adv. Immunol.*, **55**, 1-96.

Gewirth, D. (1995) *The HKL Manual*. Yale University, New Haven, Connecticut.

Glaspy, J. (1996) Clinical applications of stem

cell factor. *Curr. Opin. Hematol.*, **3**, 223-229.

Harpaz, Y. and Chothia, C. (1994) Many of the immunoglobulin superfamily domains in cell adhesion molecules and surface receptors belong to a new structural set which is close to that containing variable domains. *J. Mol. Biol.*, **238**, 528-539.

Heidaran, M. A., et al. (1990) Chimeric alpha- and beta-platelet-derived growth factor (PDGF) receptors define three immunoglobulin-like domains of the alpha-PDGF receptor that determine PDGF-AA binding specificity. *J. Biol. Chem.*, **265**, 18741-18744.

Heldin, C.-H. (1995) Dimerization of cell surface receptors in signal transduction. *Cell*, **80**, 213-223.

Hendrickson, W. A. (1979) Transformations to optimize the superposition of similar structures. *Acta Cryst*, A, **35**, 158-163.

Hendrickson, W. A. et al. (1985) Direct phase determination based on anomalous scattering. *Methods Enzymology*, **115**, 41-55.

Houck, K. A., et al. (1991) The vascular endothelial growth factor family: identification of a fourth molecular species and characterization of alternative splicing of RNA. *Mol. Endocrinol.*, **5**,

1806-1814.

Hsu, Y.-R., et al. (1996) *In vitro* methionine oxidation of Escherichia coli-derived human stem cell factor: effects on molecular structure, biological activity, and dimerization. *Protein Sci.*, **5**, 1165-1173.

Hsu, Y.-R., et al. (1998) Selective deamidation of recombinant human stem cell factor during *in vitro* aging: isolation and characterization of the aspartyl and isoaspartyl homodimers and heterodimers. *Biochemistry*, **37**, 2251-2262.

Huang, E., et al. (1990) The hematopoietic growth factor KL is encoded by the *Sl* locus and is the ligand of the c-kit receptor, the product of the *W* locus, Cell, **63**, 225-233.

Jones, D. T., et al. (1992) A new approach to protein fold recognition. *Nature*, **358**, 86-89.

Jones, E. Y., et al. (1995) Crystal structure of integrin-binding fragment of vascular cell adhesion molecule-1 at 1.8 angstroms resolution. *Nature*, **373**, 539-544.

Jones, T. A. (1992) a, yaap, asap, @#*? A set of averaging programs, In S. Bailey, Hubbard, R. & Waller, D. (ed.) *Molecular Replacement, Proceedings*

of the CCP4 Study Weekend, Daresbury Laboratory, Warrington, UK, pp. 92-105.

Jones, T. A., et al. (1991) Improved methods for building protein models in electron density maps and the location of errors in these models. *Acta Crystallogr.*, A, **47**, 110-119.

Kawasaki, E. S. and Ladner, M. B. (1990) Molecular biology of macrophage colony-stimulating factor. *Immunol. Ser.*, **49**, 155-176.

Kelvenbach, C. G., et al. (1991) Densimetric determination of carbohydrate content in glycoproteins. *J. Biochem. Biophys Methods*, **23**, 295-300.

Kleywegt, G. J. and Jones, T. A. (1994) Halloween ...masks and bones. In Bailey, S. Hubbard, R., and Waller, D. (eds), From First Map to Final Model, Proceedings of the CCP4 Study Weekend. Daresbury Laboratory, Warrington, UK, pp 59-66.

Koths, K. (1997) Structure-function studies on human macrophage colony-stimulating factor. *Mol. Reprod. Dev.*, **46**, 31-37.

Langley, K. E., et al. (1992) Purification and characterization of soluble forms of human and rat stem cell factor recombinantly expressed by *Escherichia Coli* and by Chinese hamster ovary

cells. *Arch. Biochem. Biophys.*, **295**, 21-28.

Langley, K. E., et al. (1994) Properties of variant forms of human stem cell factor recombinantly expressed in *Escherichia coli*. *Arch. Biochem. Biophys.*, **311**, 55-61.

Laskowski, R. A., et al. (1993) PROCHECK: a program to check stereochemical quality of protein structures. *J. Appl. Crystallogr.*, **26**, 283-291.

Lemmon, M.A., et al. (1997) Kit receptor dimerization is driven by bivalent of stem cell factor, *J. Biol. Chem.*, 272, 6311-6317.

Lev, S., et al., (1992) Dimerization and activation of the Kit receptor by monovalent and bivalent binding of the stem cell factor. *J. Biol. Chem.*, **267**, 15970-15977.

Lev, S., et al., (1993) Interspecies molecular chimeras of Kit help define the binding site of the stem cell factor. *Mol. Cell. Biol.*, **13**, 2224-2234.

Lev, S., et al., (1994) Steel factor and *c-kit* protooncogene: genetic lessons in sugnal transduction, *Crit. Rev. Oncog.*, **5**, 141-168.

Lu, H. S., et al., (1991) Amino acid sequence and post-translational modification of stem cell factor isolated from buffalo rat liver cell-conditioned

medium. *J. Biol. Chem.*, **266**, 8102-8107.

Lu, H. S., et al., (1992) Post-translational processing of membrane-associated recombinant human stem cell factor expressed in Chinese hamster ovary cells. *Arch. Biochem. Biophys.*, **298**, 150-158.

Lu, H. S., et al., (1996) Isolation and characterization of a disulfide-linked human stem cell factor dimer. *J. Biol. Chem.*, **271**, 11309-11316.

Lyman, S.D, and Jacobsen, S.E.W. (1998) c-Kit ligand and Flt3 ligand: stem/progenitor cell factors with overlapping yet distinct activities, Blood, **91**, 1101-1134.

Martin, F. H., et al., (1990) Primary structure and functional expression of rat and human stem cell factor DNAs. *Cell*, **63**, 203-211.

Matous, J. V., et al., (1996) Structure-function relationships of stem cell factor: an analysis based on a series of human-murine SCF chimera and the mapping of a neutralizing monoclonal antibody. *Blood*, **88**, 437-444.

McDonald, N. Q., et al., (1995) Crystal structure of dimeric human ciliary neurotrophic factor determined by MAD phasing. *EMBO J.*, **14**, 2689-2699.

McKay, D.B. (1992) Unraveling the structure of IL-2, *Science*, **257**, 412-413.

McNiece, I. K. and Briddell, R. A. (1995) Stem cell factor. *J. Leukoc. Biol.*, **57**, 14-22.

Mendiaz, E. A., et al. (1996) Epitope mapping and immunoneutralization of recombinant human stem cell factor. *Eur. J. Biochem.*, **239**, 842-849.

Milburn, M. V., et al. (1993) A novel dimer configuration revealed by the crystal structure at 2.4 Å resolution of human interleukin-5. *Nature*, **363**, 172-176.

Muller, Y. A., et al. (1997) Vascular endothelial growth factor: crystal structure and functional mapping of the kinase domain receptor binding site. *Proc. Natl. Acad. Sci. USA*, **94**, 7192-7197.

Neufeld, G., et al. (1994) Vascular endothelial growth factor and its receptors. *Prog. Growth Factor Res.*, **5**, 89-97.

Nicholls, A., et al. (1991) Protein folding and association: insights from the interfacial and thermodynamic properties of hydrocarbons. *Proteins*, **11**, 281-296.

Oefner, C., et al. (1992) Crystal structure of human platelet-derived growth factor BB. *EMBO J.*,

11, 3921-3926.

Otwinowski, Z. (1993) Oscillation data reduction program, In N.I.L. Sawyer, and S. Bailey (eds.) *Data Collection and Processing*, Science and Engineering Research Council, Warrington, UK, Vol. pp. 55-62.

Pähler, A., et al., (1990) A probability representation for phase information from multiwavelength anomalous dispersion. *Acta Cryst*, A, **46**, 537-540.

Pandit, J., et al., (1992) Three-dimensional structure of dimeric huam recombinant macrophage colony-stimulating factor. *Science*, **258**, 1358-1362.

Philo, J. S., et al., (1996) Human stem cell factor dimer forms a complex with two molecules of the extracellular domain of its receptor, Kit. *J. Biol. Chem.*, **271**, 6895-6902.

Qiu, F., et al., (1988) Primary structure of c-kit: relationship with the CSF-1/PDGF receptor kinase family-oncogenic activation of v-kit involves deletion of extracellular domain and C terminus. *EMBO J.*, **7**, 1003-1011.

Raines, E.W. and Ross, R. (1992) Compartmentalization of PDGF on extracellular binding sites dependent on exon-6-encoded

sequences. *J. Cell Biol.*, **116**, 533-543.

Read, R. J. (1986) Improved Fourier coefficients for maps using phases from partial structures with errors. *Acta Crystallogr*, A, **42**, 140-149.

Rousset, D., et al., (1995) Molecular evolution of the genes encoding receptor tyrosine kinase with immunoglobulinlike domains. *J. Mol. Evol.*, **41**, 421-430.

Rozwarski, D. A., et al., (1994) Structural comparisons among the short-chain helical cytokines. *Structure*, **2**, 159-173.

Russell, E.S. (1979) Hereditary anemias of the mouse: a review for geneticists. *Adv. Genet.*, **20**, 357-459.

Shrake, A. and Rupley, J. A. (1973) Environment and exposure to solvent of protein atoms: lysozyme and insulin. *J. Mol. Biol.*, **79**, 351-371.

Shull, R.M. et al., (1992) Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic progenitors in long-term canine marro

Stanley, E. R. and Guilbert, L. J. (1981) Methods for the purificaiton, assay, characterization and target cell binding of a colony stimulating factor (CSF-1). *J. Immunol. Methods*, **42**, 253-284.

Sprang, S.R. and Bazan J.F. (1993) Cytokine structural taxonomy and mechanisms of receptor engagement, *Curr. Opin. Struct. Biol.*, **3**, 815-827.

Stein, J., et al. (1990) Direct stimulation of cells expressing receptors for macrophage colony-stimulating factor (CSF-1) by a plasma membrane-bound precursor of human CSF-1. *Blood*, **76**, 1308-1314.

Tan, K., et al., (1998) The structure of immunoglobulin superfamily domains 1 and 2 of MAdCAM-1 reveals novel features important for integrin recognition. *Structure*, **6**, 793-801.

Taylor, E. W., et al., (1994) Structure-function studies on recombinant human macrophage colony-stimulating factor (M-CSF). *J. Biol. Chem.*, **269**, 31171-31177.

Toksoz, D., et al., (1992) Support of human hematopoiesis in long-term bone marrow cultures by murine stromal cells selectively expressing the membrane-bound and secreted forms of the human homolog of the steel gene product, stem cell factor. *Proc. Natl. Acad. Sci. USA*, **89**, 7350-7354.

Wang, J. H., et al., (1995) The crystal structure of an N-terminal two-domain fragment of vascular cell adhesion molecule 1 (VCAM-1): a cyclic peptide based on the domain 1 C-D loop can inhibit

VCAM-1-alpha 4 integrin interaction. *Proc. Natl. Acad. Sci. USA*, **92**, 5714-5718.

Wang, Z., et al., (1993) Identification of the ligand-binding regions in the macrophage colony-stimulating factor receptor extracellular domain. *Mol. Cell. Biol.*, **13**, 5348-5359.

Wiesmann, C., et al., (1997) Crystal structure at 1.7 Å resolution of VEGF in complex with domain 2 of the Flt-1 receptor. *Cell*, **91**, 695-704.

Wlodawer, A., et al., (1992) Crystal structure of human recombinant interleukin-4 at 2.25 Å, *FEBS Lett.*, **309**, 59-64.

Zdanov, A., et al., (1995) Crystal structure of interleukin-10 reveals the functional dimer with an unexpected topological similarity to interferon gamma. *Structure*, **3**, 591-601.

Zimmer, Y., et al., (1993) Multiple structural elements determine lignad binding of fibroblast growth factor receptors: Evidence that both Ig domain 2 and 3 define receptor specificity. *J. Biol. Chem.*, **268**, 7899-7903.

What is claimed is:

1. A computer based method for preparing a stem cell factor (SCF) analog comprising the steps of:

(a) providing computer expression of the three dimensional structure of an SCF molecule using its crystal structure;

(b) selecting from the computer expression of step (a) at least one site on the SCF molecule for alteration;

(c) preparing a SCF molecule having an alteration at said at least one selected site; and

(d) optionally, testing the SCF molecule for a desired characteristic.

2. The method of claim 1, wherein the SCF analog comprises a polypeptide having an amino acid sequence portion of SCF capable of binding a receptor and having the overall three-dimensional conformation as shown in Figures 2A-2B, wherein the three-dimensional conformation is:

a) anti-parallel, double-cross over 4-alpha helical bundle with a left hand twist; and

b) overall dimensions of approximately 85 Å x 30 Å x 20 Å.

3. The method of claim 1, wherein the SCF analog

comprises electron density distributions as set forth in Figures 1A, 1B, and 1C.

4. The method of claim 1 wherein the SCF molecule is a native SCF or a selenomethionyl SCF.

5. The method of claim 1 wherein the site on the SCF molecule for alteration is a receptor binding site on the surface of the SCF molecule or a non-receptor site of the SCF.

6. The method of claim 5, wherein the receptor binding site comprises approximately amino acid residues 79-95.

7. An isolated SCF analog prepared according to the method of claim 1.

8. The isolated SCF analog of claim 7, wherein the SCF analog comprises a polypeptide having an amino acid sequence portion of SCF capable of binding a receptor and having the overall three-dimensional conformation as shown in Figures 2A-2B, wherein the three-dimensional conformation is:

a) anti-parallel, double-cross over 4-alpha helical bundle with a left hand twist; and

b) overall dimensions of approximately 85 Å x 30 Å x 20 Å..

9. The isolated SCF analog of claim 10, wherein the SCF analog comprises electron density distributions altered from those set forth in Figures 1A, 1B, and 1C.

10. A composition comprising an isolated SCF analog prepared according to the method of claim 1 effective to treat a subject and a pharmaceutically acceptable carrier.

11. A method of treating a subject having a disorder requiring SCF comprising administration of a composition comprising an isolated SCF analog prepared by the method of claim 1 or a compound designed by the method of claim 32.

12. The method of claim 11, wherein the subject has a blood disorder.

13. The method of claim 12, wherein the disorder which the subject has is anemia, myeloproliferative disorder, neoplasia, nerve damage, infertility, intestinal damage, a pigmentation disorder, or immunodeficiency.

14. The method of claim 11, wherein the administration of the isolated SCF analog is for ex vivo or in vivro production of peripheral blood progenitors, ex vivo or in vivro stem cell expansion, ex vivo or in vitro

growth of epithelial cells, ex vivo or in vitro growth of stromal cells, ex vivo or in vitro dendritic cell stimulation, and in vivo cell mobilization.

15. A method for designing a compound capable of binding to the stem cell factor (SCF) receptor site of comprising the steps of:

a) determining a binding site for the SCF receptor on the SCF based on the three-dimensional structure of SCF or an SCF polypeptide or portion/fragment thereof, atomic coordinates computed from X-ray diffraction data of a crystal comprising a polypeptide having an amino acid sequence portion of SCF capable of binding the receptor; and

b) designing a compound comprising an entity that binds the SCF receptor.

16. The method of claim 15, wherein the design of the compound of step (b) is determined by shape complementarity or by estimated interaction energy.

17. The method of claim 15, wherein the designed compound fits an SCF receptor binding site on SCF receptor as shown in Figure 6.

18. The method of claim 15, wherein the designed compound fits an SCF receptor binding site on

SCF receptor as shown in Figures 7A or 7B.

19. The method of claim 15, wherein the designed compound is a double-headed SCF ligand analog having the structure set forth in Figure 10A.

20. The method of claim 19, wherein each ligand head of the double-headed SCF ligand analog is an oligopeptide having the structure set forth in Figure 10B.

21. The method of claim 20, wherein the ooligopeptide comprises a sequence, wherein functional moiety F_1 corresponds to a segment of amino acid residues from within N-terminal residues 1-10 of SCF, functional moiety F_2 corresponds to a segment of amino acid residues from within residues 79-95 of SCF, and functional moiety F_3 corresponds to a segment of amino acid residues located within three amino acid residues of amino acid residue 127, wherein F_1, F_2, and F_3 are connected by connecting peptide segements X_n, X_m, and X_p, respectively, wherein n=0-5, m=0-5 and p=3-8 amino acid residues, respectively, and the conjugation moiety F_L is a cysteine residue.

22. The method of claim 21, wherein the functional moieties F_1, F_2, and F_3 on the ligand heads have been selected by bacterial phage display

for optimal receptor binding.

23. The method of claim 21, wherein the functional moieties and connecting peptide segments of an active oligopeptide ligand head are replaced by chemical mimetics.

24. The method of claim 15, wherein an appropriate chemical scaffold of connecting segments has been designed to comprise (present) functional moieties F_1, F_2, and F_3, which have been selected by combinatorial chemistry for optimal receptor binding from a library of chemical moieties complementary to receptor-binding sites on the surface of SCF.

25. The method of claim 15, wherein the linker comprises an organic polymer having two ends capped at each end by a reactive capping moiety, F_c, which react covalently with the conjugation moiety, F_L, on the ligand head.

26. The method of claim 25, wherein the organic polymer is polyethyleneglycol (PEG) comprising the structure $H[OCH_2CH_2]_nOH$, wherein n is 10-20.

27. The method of claim 25, wherein the capping moiety, F_c, is a thiol-reactive group such as N-ethyl maleimide.

28. The method of claim 15, wherein the conjugating moiety, F_L, is a thiol containing group such as cysteine.

29. A compound designed by the method of claim 15.

30. A composition comprising the compound designed by the method of claim 15 and a pharmaceutically acceptable carrier.

31. The compound of claim 30, wherein the compound comprises an isolated SCF analog, whose alteration site is a receptor-binding site on the surface of the altered SCF molecule.

32. A method of treating a subject comprising administration of a compound designed by the method of claim 32.

33. The method of claim 32, wherein the subject has a blood disorder.

34. The method of claim 33, wherein the blood disorder is anemia or immunodeficiency.

35. The method of claim 32, wherein the compound is an isolated SCF analog.

36. A method of stimulating the production of hematopoietic cells in a subject comprising administering an isolated stem cell factor

(SCF) analog.

37. The method of claim 36, wherein isolated stem cell factor (SCF) analog is prepared by the method of claim 1 or designed by the method of claim 32.

38. The method of claim 37, wherein the isolated SCF analog comprises amino acid residues of native or recombinant SCF1-165 or amino acid residues of a recombinant selenomethionyl SCF1-141.

39. An isolated stem cell factor (SCF) molecule, which is an altered SCF, comprising any portion of amino acids 1-165 of a human SCF polypeptide, optionally comprising an N-terminal methionine before amino acid residue 1, wherein the polypeptide has an amino acid sequence portion of SCF capable of binding to the SCF receptor.

40. The altered isolated stem cell factor molecule of claim 39, wherein an alteration is selected from the group consisting of deletion, insertion and substitution of at least one amino acid residue from the naturally occurring amino acid sequence of SCF.

41. The altered isolated stem cell factor molecule of claim 40, wherein an alteration is a

truncated SCF comprising amino acids 1-141 of a human SCF polypeptide, optionally comprising an N-terminal methionine before amino acid residue 1.

42. The altered isolated stem cell factor molecule of claim 40, wherein the substitution of at least one amino acid residue is selected from the group consisting of SCF(Y26C) disulfide-linked dimer, SCF(D25C), SCF(K62C), SCF(K78N, N81K), SCF(R117A, I118A), SCF(E92A, S95A), and SCF(D124A, K127D).

43. A stem cell factor molecule of claim 40, wherein the overall three-dimensional conformation of the stem cell factor molecule has an altered three-dimensional structure of the αC-β2 loop.

44. A pharmaceutical composition comprising the altered isolated SCF molecule of claim 39 and a pharmaceutically acceptable carrier.

45. A stem cell factor molecule of claim 39, wherein the molecule is a hybrid molecule of the altered stem cell factor molecule and a second protein or fragment thereof.

46. A stem cell factor molecule of claim 39, wherein the alteration of the αC-β2 loop is a change in length of the amino acid sequence of

the αC-β2 loop by a deletion or an insertion of at least one amino acid residue or a change in at least one amino acid residue from the naturally occurring amino acid residue(s) of the αC-β2 loop.

47. The altered isolated stem cell factor molecule of claim 46, wherein the change in said at least one amino acid residue from the naturally occurring amino acid residue(s) is selected from the group consisting of SCF(Y26C) disulfide-linked dimer, SCF(D25C), SCF(K62C), SCF(K78N, N81K), SCF(R117A, I118A), SCF(E92A, S95A), and SCF(D124A, K127D).

CONJUGATED LIGANDS FOR THE STIMULATION OF BLOOD CELL PROLIFERATION BY EFFECTING DIMERIZATION OF THE RECEPTOR FOR STEM CELL FACTOR

ABSTRACT OF THE DISCLOSURE

This invention provides a computer based method for preparing a stem cell factor (SCF) analog comprising the steps of: (a) providing computer expression of the three dimensional structure of an SCF molecule using its crystal structure; (b) selecting from the computer expression of step (a) at least one site on the SCF molecule for alteration; (c) preparing a SCF molecule having an alteration at said at least one selected site; and (d) optionally, testing the SCF molecule for a desired characteristic. This invention also provides SCF analogs and SCF ligand analogs prepared according to the above-described method. Compositions comprising SCF analogs or SCF ligand analogs prepared according to the above-described method effective to treat a subject and a pharmaceutically acceptable carrier are provided, as are methods of treating a subject comprising administration of pharmaceutical compositions comprising the prepared SCF analogs and SCF ligand analogs prepared by the described methods. This invention also provides methods for designing compounds capable of binding to the SCF receptor site and compounds designed by the above-descibed methods.

Figure 1

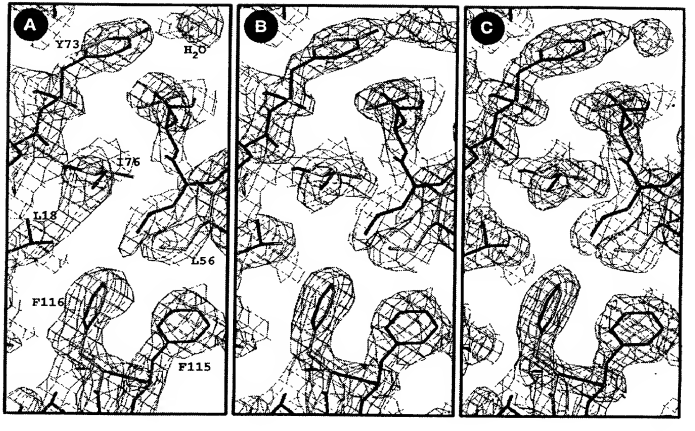

Figure 2

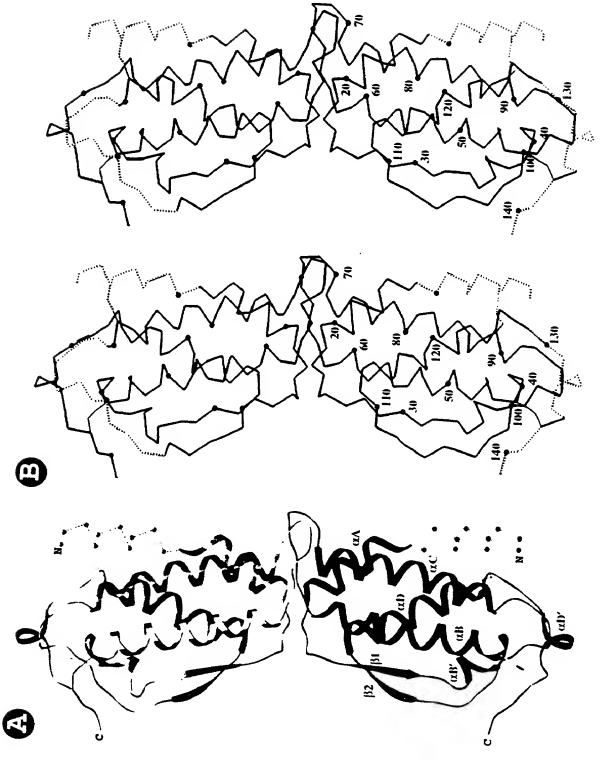
B
70
20
60
80
120
90
130
110
30
50
40
100
140
A
N
αA
αC
αD
αE
αF
β1
β2
αB
C

Figure 3

Figure 4

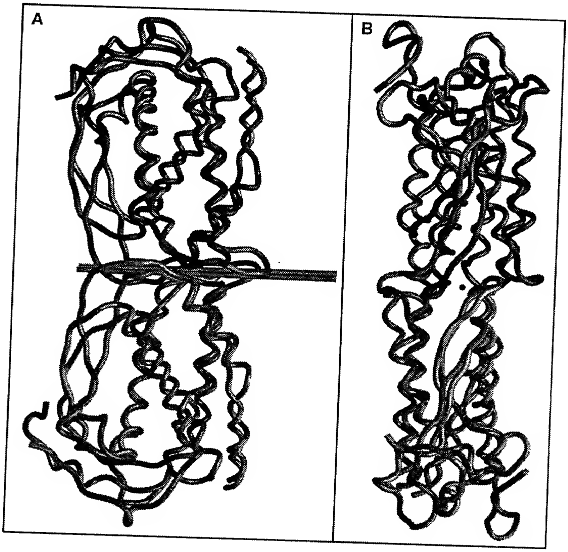

Figure 5

Figure 6

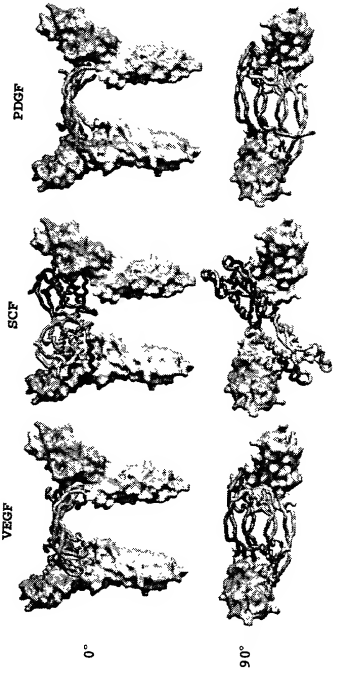

Figure 7

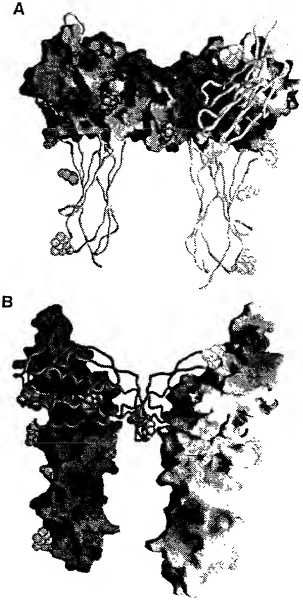

Figure 8-1

```
HEADER    GROWTH FACTOR                                                 1SCF
TITLE     HUMAN RECOMBINANT STEM CELL FACTOR
COMPND    MOL_ID: 1;
COMPND   2 MOLECULE: STEM CELL FACTOR;
COMPND   3 CHAIN: A, B, C, D;
COMPND   4 SYNONYM: SCF, SL, MGF, MAST CELL GROWTH FACTOR;
COMPND   5 ENGINEERED: YES;
COMPND   6 BIOLOGICAL_UNIT: DIMER
SOURCE    MOL_ID: 1;
SOURCE   2 ORGANISM_SCIENTIFIC: HOMO SAPIENS;
SOURCE   3 ORGANISM_COMMON: HUMAN;
SOURCE   4 EXPRESSION_SYSTEM: NULL
KEYWDS    HUMAN STEM CELL FACTOR, STEEL FACTOR, KIT LIGAND, MAST CELL
KEYWDS   2 GROWTH FACTOR
EXPDTA    X-RAY DIFFRACTION
AUTHOR    X.JIANG,O.GUREL,K.E.LANGLEY,W.A.HENDRICKSON
JRNL        AUTH    X.JIANG,O.GUREL,K.E.LANGLEY,W.A.HENDRICKSON
JRNL        TITL    CRYSTAL STRUCTURE OF RECOMBINANT HUMAN STEM CELL
JRNL        TITL 2 FACTOR
JRNL        REF     TO BE PUBLISHED
JRNL        REFN                                                        0353
REMARK   1
REMARK   2
REMARK   2 RESOLUTION. 2.2  ANGSTROMS.
REMARK   3
REMARK   3 REFINEMENT.
REMARK   3   PROGRAM     : X-PLOR 3.1
REMARK   3   AUTHORS     : BRUNGER
REMARK   3
REMARK   3  DATA USED IN REFINEMENT.
REMARK   3   RESOLUTION RANGE HIGH (ANGSTROMS) : 2.2
REMARK   3   RESOLUTION RANGE LOW  (ANGSTROMS) : 20.0
REMARK   3   DATA CUTOFF            (SIGMA(F)) : 2
REMARK   3   DATA CUTOFF HIGH         (ABS(F)) : 100000
REMARK   3   DATA CUTOFF LOW          (ABS(F)) : 0.1
REMARK   3   COMPLETENESS (WORKING+TEST)   (%) : 96.6
REMARK   3   NUMBER OF REFLECTIONS             : 49851
REMARK   3
REMARK   3  FIT TO DATA USED IN REFINEMENT.
REMARK   3   CROSS-VALIDATION METHOD       : THROUGHOUT
REMARK   3   FREE R VALUE TEST SET SELECTION  : RANDOM
REMARK   3   R VALUE            (WORKING SET) : 0.199
REMARK   3   FREE R VALUE                     : 0.242
REMARK   3   FREE R VALUE TEST SET SIZE   (%) : 6.0
REMARK   3   FREE R VALUE TEST SET COUNT      : 3016
REMARK   3   ESTIMATED ERROR OF FREE R VALUE  : 0.0044
REMARK   3
REMARK   3  FIT IN THE HIGHEST RESOLUTION BIN.
REMARK   3   TOTAL NUMBER OF BINS USED           : 10
REMARK   3   BIN RESOLUTION RANGE HIGH       (A) : 2.0
REMARK   3   BIN RESOLUTION RANGE LOW        (A) : 2.28
REMARK   3   BIN COMPLETENESS (WORKING+TEST) (%) : 97.0
REMARK   3   REFLECTIONS IN BIN    (WORKING SET) : 4349
REMARK   3   BIN R VALUE           (WORKING SET) : 0.3159
REMARK   3   BIN FREE R VALUE                    : 0.3450
REMARK   3   BIN FREE R VALUE TEST SET SIZE  (%) : 6.4
REMARK   3   BIN FREE R VALUE TEST SET COUNT     : 302
REMARK   3   ESTIMATED ERROR OF BIN FREE R VALUE : 0.0198
REMARK   3
REMARK   3  NUMBER OF NON-HYDROGEN ATOMS USED IN REFINEMENT.
```

Figure 8-2

```
REMARK   3    PROTEIN ATOMS            : 3517
REMARK   3    NUCLEIC ACID ATOMS       : 0
REMARK   3    HETEROGEN ATOMS          : 19
REMARK   3    SOLVENT ATOMS            : 264
REMARK   3
REMARK   3  B VALUES.
REMARK   3    FROM WILSON PLOT              (A**2) : 38.5
REMARK   3    MEAN B VALUE      (OVERALL, A**2) : 32.1
REMARK   3    OVERALL ANISOTROPIC B VALUE.
REMARK   3     B11 (A**2) : NULL
REMARK   3     B22 (A**2) : NULL
REMARK   3     B33 (A**2) : NULL
REMARK   3     B12 (A**2) : NULL
REMARK   3     B13 (A**2) : NULL
REMARK   3     B23 (A**2) : NULL
REMARK   3
REMARK   3  ESTIMATED COORDINATE ERROR.
REMARK   3    ESD FROM LUZZATI PLOT         (A) : NULL
REMARK   3    ESD FROM SIGMAA               (A) : NULL
REMARK   3    LOW RESOLUTION CUTOFF         (A) : NULL
REMARK   3
REMARK   3  CROSS-VALIDATED ESTIMATED COORDINATE ERROR.
REMARK   3    ESD FROM C-V LUZZATI PLOT     (A) : NULL
REMARK   3    ESD FROM C-V SIGMAA           (A) : NULL
REMARK   3
REMARK   3  RMS DEVIATIONS FROM IDEAL VALUES.
REMARK   3    BOND LENGTHS                  (A) : 0.016
REMARK   3    BOND ANGLES            (DEGREES) : 2.5
REMARK   3    DIHEDRAL ANGLES        (DEGREES) : 22.8
REMARK   3    IMPROPER ANGLES        (DEGREES) : 2.05
REMARK   3
REMARK   3  ISOTROPIC THERMAL MODEL : RESTRAINED
REMARK   3
REMARK   3  ISOTROPIC THERMAL FACTOR RESTRAINTS.    RMS    SIGMA
REMARK   3    MAIN-CHAIN BOND               (A**2) : 1.2   ; 1.5
REMARK   3    MAIN-CHAIN ANGLE              (A**2) : 1.6   ; 2.0
REMARK   3    SIDE-CHAIN BOND               (A**2) : 2.1   ; 2.0
REMARK   3    SIDE-CHAIN ANGLE              (A**2) : 2.4   ; 2.5
REMARK   3
REMARK   3  NCS MODEL : RESTRAINTS
REMARK   3
REMARK   3  NCS RESTRAINTS.                          RMS   SIGMA/WEIGHT
REMARK   3    GROUP  1  POSITIONAL              (A) : NULL  ; NULL
REMARK   3    GROUP  1  B-FACTOR           (A**2) : NULL  ; NULL
REMARK   3
REMARK   3  PARAMETER FILE  1  : PARAM19_MOD.PRO
REMARK   3  PARAMETER FILE  2  : PARAM19.SOL
REMARK   3  PARAMETER FILE  3  : HETEROPARAM19.PAR
REMARK   3  TOPOLOGY FILE  1   : TOPH19_MOD.PRO
REMARK   3  TOPOLOGY FILE  2   : TOPH19.SOL
REMARK   3  TOPOLOGY FILE  3   : HETERO.TOP
REMARK   3
REMARK   3  OTHER REFINEMENT REMARKS: REFINEMENT WAS PERFORMED WITH
REMARK   3  ANOMALOUS ON; PARAM19_MOD.PRO AND TOPH19_MOD.PRO ARE
REMARK   3  MODIFIED PARAMETER AND TOPOLOGY FILES OF PARAM19.PRO AND
REMARK   3  TOPH19.PRO, RESPECTIVELY, FOR SELENOMETHIONYL PROTEINS.
REMARK   3  NCS RESTRAINTS WERE APPLIED ONLY DURING THE INITIAL
REMARK   3  REFINEMENT.
REMARK   4
REMARK   4 1SCF COMPLIES WITH FORMAT V. 2.3,
```

Figure 8-3

```
REMARK   6
REMARK   6 THE FOLLOWING RESIDUES ARE DISORDERED IN THE STRUCTURE:
REMARK   6 A1-10; A92-103; B1-10; B130-136; B139-141; C1-10; C92-103;
REMARK   6 C127-141; D1-10; D91-103; D128-141
REMARK   7
REMARK   7 THE SIDE CHAINS OF THE FOLLOWING RESIDUES ARE DISORDERED IN
REMARK   7 THE STRUCTURE: A11-13,A91,A127,A133,B11,B13,B93,B96-97,
REMARK   7 B103,B128,B137,C11,C13,C39,D11,D13,D90,D106,D127
REMARK   8
REMARK   8 LYS A 91 IS LAST RESIDUE BEFORE GAP, PHE B 129 IS LAST
REMARK   8 RESIDUE BEFORE GAP, LYS C 91 IS LAST RESIDUE BEFORE GAP,
REMARK   8 PHE C 126 IS LAST RESIDUE BEFORE GAP, VAL D 90 IS LAST
REMARK   8 RESIDUE BEFORE GAP.
REMARK 200
REMARK 200 EXPERIMENTAL DETAILS
REMARK 200  EXPERIMENT TYPE                : X-RAY DIFFRACTION
REMARK 200  DATE OF DATA COLLECTION        :
REMARK 200  TEMPERATURE           (KELVIN) : 110
REMARK 200  PH                             : 7.4
REMARK 200  NUMBER OF CRYSTALS USED        : 1
REMARK 200
REMARK 200  SYNCHROTRON              (Y/N) : Y
REMARK 200  RADIATION SOURCE               : NSLS
REMARK 200  BEAMLINE                       : X4A
REMARK 200  X-RAY GENERATOR MODEL          : NULL
REMARK 200  MONOCHROMATIC OR LAUE    (M/L) : M
REMARK 200  WAVELENGTH OR RANGE        (A) : 0.986
REMARK 200  MONOCHROMATOR                  : SILICON CRYSTAL
REMARK 200  OPTICS                         : MIRRORS
REMARK 200
REMARK 200  DETECTOR TYPE                  : IMAGE PLATE
REMARK 200  DETECTOR MANUFACTURER          : FUJI
REMARK 200  INTENSITY-INTEGRATION SOFTWARE : DENSO
REMARK 200  DATA SCALING SOFTWARE          : SCALEPACK
REMARK 200
REMARK 200  NUMBER OF UNIQUE REFLECTIONS   : 65689
REMARK 200  RESOLUTION RANGE HIGH      (A) : 2.0
REMARK 200  RESOLUTION RANGE LOW       (A) : 25
REMARK 200  REJECTION CRITERIA  (SIGMA(I)) : -3
REMARK 200
REMARK 200 OVERALL.
REMARK 200  COMPLETENESS FOR RANGE     (%) : 94.9
REMARK 200  DATA REDUNDANCY                : 2.75
REMARK 200  R MERGE                    (I) : NULL
REMARK 200  R SYM                      (I) : 0.056
REMARK 200  <I/SIGMA(I)> FOR THE DATA SET  : 15.3
REMARK 200
REMARK 200 IN THE HIGHEST RESOLUTION SHELL.
REMARK 200  HIGHEST RESOLUTION SHELL, RANGE HIGH (A) : 2.0
REMARK 200  HIGHEST RESOLUTION SHELL, RANGE LOW  (A) : 2.07
REMARK 200  COMPLETENESS FOR SHELL     (%) : 72
REMARK 200  DATA REDUNDANCY IN SHELL       : 2.23
REMARK 200  R MERGE FOR SHELL          (I) : NULL
REMARK 200  R SYM FOR SHELL            (I) : 0.581
REMARK 200  <I/SIGMA(I)> FOR SHELL         : 1.6
REMARK 200
REMARK 200 DIFFRACTION PROTOCOL: NULL
REMARK 200 METHOD USED TO DETERMINE THE STRUCTURE: MAD
REMARK 200 SOFTWARE USED: MADLSQ
REMARK 200 STARTING MODEL: NULL
```

Figure 8-4

```
REMARK 200
REMARK 200 REMARK: NULL
REMARK 280
REMARK 280 CRYSTAL
REMARK 280 SOLVENT CONTENT, VS   (%): NULL
REMARK 280 MATTHEWS COEFFICIENT, VM (ANGSTROMS**3/DA): NULL
REMARK 280
REMARK 280 CRYSTALLIZATION CONDITIONS: PROTEIN WAS CRYSTALLIZED FROM
REMARK 280 22% PEG 400, 220 MM CACL2, 100 MM HEPES, PH 7.4 AND 5MM
REMARK 280 DTT IN 20 DEGREE ROOM
REMARK 290
REMARK 290 CRYSTALLOGRAPHIC SYMMETRY
REMARK 290 SYMMETRY OPERATORS FOR SPACE GROUP: P 21 21 21
REMARK 290
REMARK 290      SYMOP   SYMMETRY
REMARK 290     NNNMMM   OPERATOR
REMARK 290       1555   X,Y,Z
REMARK 290       2555   1/2-X,-Y,1/2+Z
REMARK 290       3555   -X,1/2+Y,1/2-Z
REMARK 290       4555   1/2+X,1/2-Y,-Z
REMARK 290
REMARK 290     WHERE NNN -> OPERATOR NUMBER
REMARK 290           MMM -> TRANSLATION VECTOR
REMARK 290
REMARK 290 CRYSTALLOGRAPHIC SYMMETRY TRANSFORMATIONS
REMARK 290 THE FOLLOWING TRANSFORMATIONS OPERATE ON THE ATOM/HETATM
REMARK 290 RECORDS IN THIS ENTRY TO PRODUCE CRYSTALLOGRAPHICALLY
REMARK 290 RELATED MOLECULES.
REMARK 290   SMTRY1   1  1.000000  0.000000  0.000000         0.00000
REMARK 290   SMTRY2   1  0.000000  1.000000  0.000000         0.00000
REMARK 290   SMTRY3   1  0.000000  0.000000  1.000000         0.00000
REMARK 290   SMTRY1   2 -1.000000  0.000000  0.000000        35.90922
REMARK 290   SMTRY2   2  0.000000 -1.000000  0.000000         0.00000
REMARK 290   SMTRY3   2  0.000000  0.000000  1.000000        44.09560
REMARK 290   SMTRY1   3 -1.000000  0.000000  0.000000         0.00000
REMARK 290   SMTRY2   3  0.000000  1.000000  0.000000        41.27456
REMARK 290   SMTRY3   3  0.000000  0.000000 -1.000000        44.09560
REMARK 290   SMTRY1   4  1.000000  0.000000  0.000000        35.90922
REMARK 290   SMTRY2   4  0.000000 -1.000000  0.000000        41.27456
REMARK 290   SMTRY3   4  0.000000  0.000000 -1.000000         0.00000
REMARK 290
REMARK 290 REMARK: NULL
REMARK 295
REMARK 295 NON-CRYSTALLOGRAPHIC SYMMETRY
REMARK 295 THE TRANSFORMATIONS PRESENTED ON THE MTRIX RECORDS BELOW
REMARK 295 DESCRIBE NON-CRYSTALLOGRAPHIC RELATIONSHIPS AMONG ATOMS
REMARK 295 IN THIS ENTRY.  APPLYING THE APPROPRIATE MTRIX
REMARK 295 TRANSFORMATION TO THE RESIDUES LISTED FIRST WILL YIELD
REMARK 295 APPROXIMATE COORDINATES FOR THE RESIDUES LISTED SECOND.
REMARK 295 CHAIN IDENTIFIERS GIVEN AS "?" REFER TO CHAINS FOR WHICH
REMARK 295 ATOMS ARE NOT FOUND IN THIS ENTRY.
REMARK 295
REMARK 295              APPLIED TO            TRANSFORMED TO
REMARK 295   TRANSFORM CHAIN  RESIDUES        CHAIN  RESIDUES      RMSD
REMARK 295     SSS
REMARK 295    M  1       B   11 ..  91         A    11 ..  91     1.020
REMARK 295    M  2       A   11 ..  91         C    11 ..  91     1.677
REMARK 295    M  3       D   11 ..  91         A    11 ..  91     1.926
REMARK 295    M  4       C   11 ..  91         B    11 ..  91     0.620
REMARK 295    M  5       D   11 ..  91         B    11 ..  91     1.764
```

Figure 8-5

```
REMARK 295     M  6        D   11 ..  91         C    11 ..  91      1.810
REMARK 295     M  7        C   11 ..  91         A    11 ..  91      0.898
REMARK 295
REMARK 295     WHERE SSS -> COLUMNS 8-10 OF MTRIX RECORDS
REMARK 295
REMARK 295 REMARK:
REMARK 295 TRANSFORMATION RELATES CHAIN B TO CHAIN A; INCLUDING
REMARK 295  RESIDUES 11-90 AND 104-126.
REMARK 295 TRANSFORMATION RELATES CHAIN C TO CHAIN A; INCLUDING
REMARK 295  RESIDUES 11-90 AND 104-126.
REMARK 295 TRANSFORMATION RELATES CHAIN D TO CHAIN A; INCLUDING
REMARK 295  RESIDUES 11-90 AND 104-126.
REMARK 295 TRANSFORMATION RELATES CHAIN C TO CHAIN B; INCLUDING
REMARK 295  RESIDUES 11-90 AND 104-126.
REMARK 295 TRANSFORMATION RELATES CHAIN D TO CHAIN B; INCLUDING
REMARK 295  RESIDUES 11-90 AND 104-126.
REMARK 295 TRANSFORMATION RELATES CHAIN D TO CHAIN C; INCLUDING
REMARK 295  RESIDUES 11-90 AND 104-126.
REMARK 295 TRANSFORMATION RELATES CHAIN CD DIMER TO CHAIN AB DIMER;
REMARK 295  INCLUDING RESIDUES A11-91,A104-126,B11-B90,B104-127,
REMARK 295  C11-91,C104-126,D11-90,D104-127
REMARK 470
REMARK 470 MISSING ATOM
REMARK 470 THE FOLLOWING RESIDUES HAVE MISSING ATOMS (M=MODEL NUMBER;
REMARK 470 RES=RESIDUE NAME; C=CHAIN IDENTIFIER; SSEQ=SEQUENCE NUMBER;
REMARK 470 I=INSERTION CODE):
REMARK 470   M RES CSSEQI  ATOMS
REMARK 470     ASN A  11    CG   OD1  ND2
REMARK 470     VAL A  12    CG1  CG2
REMARK 470     LYS A  13    CG   CD   CE   NZ
REMARK 470     LYS A  91    CG   CD   CE   NZ
REMARK 470     LYS A 127    CG   CD   CE   NZ
REMARK 470     SER A 133    OG
REMARK 470     ASN B  11    CG   OD1  ND2
REMARK 470     LYS B  13    CG   CD   CE   NZ
REMARK 470     ASN B  93    CG   OD1  ND2
REMARK 470     LYS B  96    CG   CD   CE   NZ
REMARK 470     ASP B  97    CG   OD1  OD2
REMARK 470     LYS B 103    CG   CD   CE   NZ
REMARK 470     ASP B 128    CG   OD1  OD2
REMARK 470     ASP B 137    CG   OD1  OD2
REMARK 470     ASN C  11    CG   OD1  ND2
REMARK 470     LYS C  13    CG   CD   CE   NZ
REMARK 470     LEU C  39    CG   CD1  CD2
REMARK 470     ASN D  11    CG   OD1  ND2
REMARK 470     LYS D  13    CG   CD   CE   NZ
REMARK 470     VAL D  90    CG1  CG2
REMARK 470     GLU D 106    CG   CD   OE1  OE2
REMARK 470     LYS D 127    CG   CD   CE   NZ
REMARK 500
REMARK 500 GEOMETRY AND STEREOCHEMISTRY
REMARK 500 SUBTOPIC: CLOSE CONTACTS
REMARK 500
REMARK 500 THE FOLLOWING ATOMS THAT ARE RELATED BY CRYSTALLOGRAPHIC
REMARK 500 SYMMETRY ARE IN CLOSE CONTACT.  AN ATOM LOCATED WITHIN 0.15
REMARK 500 ANGSTROMS OF A SYMMETRY RELATED ATOM IS ASSUMED TO BE ON A
REMARK 500 SPECIAL POSITION AND IS, THEREFORE, LISTED IN REMARK 375
REMARK 500 INSTEAD OF REMARK 500.  ATOMS WITH NON-BLANK ALTERNATE
REMARK 500 LOCATION INDICATORS ARE NOT INCLUDED IN THE CALCULATIONS.
REMARK 500
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Figure 8-6

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REMARK 500 DISTANCE CUTOFF:
REMARK 500 2.2 ANGSTROMS FOR CONTACTS NOT INVOLVING HYDROGEN ATOMS
REMARK 500 1.6 ANGSTROMS FOR CONTACTS INVOLVING HYDROGEN ATOMS
REMARK 500
REMARK 500  ATM1  RES C  SSEQI    ATM2  RES C  SSEQI   SSYMOP    DISTANCE
REMARK 500  CA     CA     1021     O     VAL A   139     3655      2.18
REMARK 500
REMARK 500 REMARK: NULL
REMARK 600
REMARK 600 HETEROGEN
REMARK 600  1PE: ONLY PART OF THE PEG400 CHAIN IS ORDERED IN THE
REMARK 600  STRUCTURE.
REMARK 999
REMARK 999 SEQUENCE
REMARK 999 1SCF  A     SWS      P21583       1 -    35 NOT IN ATOMS LIST
REMARK 999 1SCF  A     SWS      P21583     167 -   273 NOT IN ATOMS LIST
REMARK 999 1SCF  B     SWS      P21583       1 -    35 NOT IN ATOMS LIST
REMARK 999 1SCF  B     SWS      P21583     164 -   273 NOT IN ATOMS LIST
REMARK 999 1SCF  C     SWS      P21583       1 -    35 NOT IN ATOMS LIST
REMARK 999 1SCF  C     SWS      P21583     152 -   273 NOT IN ATOMS LIST
REMARK 999 1SCF  D     SWS      P21583       1 -    35 NOT IN ATOMS LIST
REMARK 999 1SCF  D     SWS      P21583     153 -   273 NOT IN ATOMS LIST
DBREF  1SCF A    11     91  SWS    P21583    SCF_HUMAN       36    116
DBREF  1SCF A   104    141  SWS    P21583    SCF_HUMAN      129    166
DBREF  1SCF B    11    129  SWS    P21583    SCF_HUMAN       36    154
DBREF  1SCF B   137    138  SWS    P21583    SCF_HUMAN      162    163
DBREF  1SCF C    11     91  SWS    P21583    SCF_HUMAN       36    116
DBREF  1SCF C   104    126  SWS    P21583    SCF_HUMAN      129    151
DBREF  1SCF D    11     90  SWS    P21583    SCF_HUMAN       36    115
DBREF  1SCF D   104    127  SWS    P21583    SCF_HUMAN      129    152
SEQADV 1SCF MSE A   27  SWS  P21583    MET    52 MODIFIED
SEQADV 1SCF MSE A   36  SWS  P21583    MET    61 MODIFIED
SEQADV 1SCF MSE A   48  SWS  P21583    MET    73 MODIFIED
SEQADV 1SCF      A      SWS  P21583    GLU   117 GAP IN PDB ENTRY
SEQADV 1SCF      A      SWS  P21583    ASN   118 GAP IN PDB ENTRY
SEQADV 1SCF      A      SWS  P21583    SER   119 GAP IN PDB ENTRY
SEQADV 1SCF      A      SWS  P21583    SER   120 GAP IN PDB ENTRY
SEQADV 1SCF      A      SWS  P21583    LYS   121 GAP IN PDB ENTRY
SEQADV 1SCF      A      SWS  P21583    ASP   122 GAP IN PDB ENTRY
SEQADV 1SCF      A      SWS  P21583    LEU   123 GAP IN PDB ENTRY
SEQADV 1SCF      A      SWS  P21583    LYS   124 GAP IN PDB ENTRY
SEQADV 1SCF      A      SWS  P21583    LYS   125 GAP IN PDB ENTRY
SEQADV 1SCF      A      SWS  P21583    SER   126 GAP IN PDB ENTRY
SEQADV 1SCF      A      SWS  P21583    PHE   127 GAP IN PDB ENTRY
SEQADV 1SCF      A      SWS  P21583    LYS   128 GAP IN PDB ENTRY
SEQADV 1SCF MSE B   27  SWS  P21583    MET    52 MODIFIED
SEQADV 1SCF MSE B   36  SWS  P21583    MET    61 MODIFIED
SEQADV 1SCF MSE B   48  SWS  P21583    MET    73 MODIFIED
SEQADV 1SCF      B      SWS  P21583    VAL   155 GAP IN PDB ENTRY
SEQADV 1SCF      B      SWS  P21583    VAL   156 GAP IN PDB ENTRY
SEQADV 1SCF      B      SWS  P21583    ALA   157 GAP IN PDB ENTRY
SEQADV 1SCF      B      SWS  P21583    SER   158 GAP IN PDB ENTRY
SEQADV 1SCF      B      SWS  P21583    GLU   159 GAP IN PDB ENTRY
SEQADV 1SCF      B      SWS  P21583    THR   160 GAP IN PDB ENTRY
SEQADV 1SCF      B      SWS  P21583    SER   161 GAP IN PDB ENTRY
SEQADV 1SCF MSE C   27  SWS  P21583    MET    52 MODIFIED
SEQADV 1SCF MSE C   36  SWS  P21583    MET    61 MODIFIED
SEQADV 1SCF MSE C   48  SWS  P21583    MET    73 MODIFIED
SEQADV 1SCF      C      SWS  P21583    GLU   117 GAP IN PDB ENTRY
SEQADV 1SCF      C      SWS  P21583    ASN   118 GAP IN PDB ENTRY
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Figure 8-7

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SEQADV 1SCF      C         SWS  P21583    SER   119 GAP IN PDB ENTRY
SEQADV 1SCF      C         SWS  P21583    SER   120 GAP IN PDB ENTRY
SEQADV 1SCF      C         SWS  P21583    LYS   121 GAP IN PDB ENTRY
SEQADV 1SCF      C         SWS  P21583    ASP   122 GAP IN PDB ENTRY
SEQADV 1SCF      C         SWS  P21583    LEU   123 GAP IN PDB ENTRY
SEQADV 1SCF      C         SWS  P21583    LYS   124 GAP IN PDB ENTRY
SEQADV 1SCF      C         SWS  P21583    LYS   125 GAP IN PDB ENTRY
SEQADV 1SCF      C         SWS  P21583    SER   126 GAP IN PDB ENTRY
SEQADV 1SCF      C         SWS  P21583    PHE   127 GAP IN PDB ENTRY
SEQADV 1SCF      C         SWS  P21583    LYS   128 GAP IN PDB ENTRY
SEQADV 1SCF MSE  D   27    SWS  P21583    MET    52 MODIFIED
SEQADV 1SCF MSE  D   36    SWS  P21583    MET    61 MODIFIED
SEQADV 1SCF MSE  D   48    SWS  P21583    MET    73 MODIFIED
SEQADV 1SCF      D         SWS  P21583    LYS   116 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    GLU   117 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    ASN   118 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    SER   119 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    SER   120 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    LYS   121 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    ASP   122 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    LEU   123 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    LYS   124 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    LYS   125 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    SER   126 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    PHE   127 GAP IN PDB ENTRY
SEQADV 1SCF      D         SWS  P21583    LYS   128 GAP IN PDB ENTRY
SEQRES   1 A  273  MET LYS LYS THR GLN THR TRP ILE LEU THR CYS ILE TYR
SEQRES   2 A  273  LEU GLN LEU LEU LEU LEU PHE ASN PRO LEU VAL LYS THR GLU
SEQRES   3 A  273  GLY ILE CYS ARG ASN ARG VAL THR ASN ASN VAL LYS ASP
SEQRES   4 A  273  VAL THR LYS LEU VAL ALA ASN LEU PRO LYS ASP TYR MSE
SEQRES   5 A  273  ILE THR LEU LYS TYR VAL PRO GLY MSE ASP VAL LEU PRO
SEQRES   6 A  273  SER HIS CYS TRP ILE SER GLU MSE VAL VAL GLN LEU SER
SEQRES   7 A  273  ASP SER LEU THR ASP LEU LEU ASP LYS PHE SER ASN ILE
SEQRES   8 A  273  SER GLU GLY LEU SER ASN TYR SER ILE ILE ASP LYS LEU
SEQRES   9 A  273  VAL ASN ILE VAL ASP ASP LEU VAL GLU CYS VAL LYS GLU
SEQRES  10 A  273  ASN SER SER LYS ASP LEU LYS LYS SER PHE LYS SER PRO
SEQRES  11 A  273  GLU PRO ARG LEU PHE THR PRO GLU GLU PHE PHE ARG ILE
SEQRES  12 A  273  PHE ASN ARG SER ILE ASP ALA PHE LYS ASP PHE VAL VAL
SEQRES  13 A  273  ALA SER GLU THR SER ASP CYS VAL VAL SER SER THR LEU
SEQRES  14 A  273  SER PRO GLU LYS ASP SER ARG VAL SER VAL THR LYS PRO
SEQRES  15 A  273  PHE MET LEU PRO PRO VAL ALA ALA SER SER LEU ARG ASN
SEQRES  16 A  273  ASP SER SER SER SER ASN ARG LYS ALA LYS ASN PRO PRO
SEQRES  17 A  273  GLY ASP SER SER LEU HIS TRP ALA ALA MET ALA LEU PRO
SEQRES  18 A  273  ALA LEU PHE SER LEU ILE ILE GLY PHE ALA PHE GLY ALA
SEQRES  19 A  273  LEU TYR TRP LYS LYS ARG GLN PRO SER LEU THR ARG ALA
SEQRES  20 A  273  VAL GLU ASN ILE GLN ILE ASN GLU GLU ASP ASN GLU ILE
SEQRES  21 A  273  SER MET LEU GLN GLU LYS GLU ARG GLU PHE GLN GLU VAL
SEQRES   1 B  273  MET LYS LYS THR GLN THR TRP ILE LEU THR CYS ILE TYR
SEQRES   2 B  273  LEU GLN LEU LEU LEU PHE ASN PRO LEU VAL LYS THR GLU
SEQRES   3 B  273  GLY ILE CYS ARG ASN ARG VAL THR ASN ASN VAL LYS ASP
SEQRES   4 B  273  VAL THR LYS LEU VAL ALA ASN LEU PRO LYS ASP TYR MSE
SEQRES   5 B  273  ILE THR LEU LYS TYR VAL PRO GLY MSE ASP VAL LEU PRO
SEQRES   6 B  273  SER HIS CYS TRP ILE SER GLU MSE VAL VAL GLN LEU SER
SEQRES   7 B  273  ASP SER LEU THR ASP LEU LEU ASP LYS PHE SER ASN ILE
SEQRES   8 B  273  SER GLU GLY LEU SER ASN TYR SER ILE ILE ASP LYS LEU
SEQRES   9 B  273  VAL ASN ILE VAL ASP ASP LEU VAL GLU CYS VAL LYS GLU
SEQRES  10 B  273  ASN SER SER LYS ASP LEU LYS LYS SER PHE LYS SER PRO
SEQRES  11 B  273  GLU PRO ARG LEU PHE THR PRO GLU GLU PHE PHE ARG ILE
SEQRES  12 B  273  PHE ASN ARG SER ILE ASP ALA PHE LYS ASP PHE VAL VAL
SEQRES  13 B  273  ALA SER GLU THR SER ASP CYS VAL VAL SER SER THR LEU
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Figure 8-8

```
SEQRES  14 B  273  SER PRO GLU LYS ASP SER ARG VAL SER VAL THR LYS PRO
SEQRES  15 B  273  PHE MET LEU PRO PRO VAL ALA ALA SER SER LEU ARG ASN
SEQRES  16 B  273  ASP SER SER SER SER ASN ARG LYS ALA LYS ASN PRO PRO
SEQRES  17 B  273  GLY ASP SER SER LEU HIS TRP ALA ALA MET ALA LEU PRO
SEQRES  18 B  273  ALA LEU PHE SER LEU ILE ILE GLY PHE ALA PHE GLY ALA
SEQRES  19 B  273  LEU TYR TRP LYS LYS ARG GLN PRO SER LEU THR ARG ALA
SEQRES  20 B  273  VAL GLU ASN ILE GLN ILE ASN GLU GLU ASP ASN GLU ILE
SEQRES  21 B  273  SER MET LEU GLN GLU LYS GLU ARG GLU PHE GLN GLU VAL
SEQRES   1 C  273  MET LYS LYS THR GLN THR TRP ILE LEU THR CYS ILE TYR
SEQRES   2 C  273  LEU GLN LEU LEU LEU PHE ASN PRO LEU VAL LYS THR GLU
SEQRES   3 C  273  GLY ILE CYS ARG ASN ARG VAL THR ASN ASN VAL LYS ASP
SEQRES   4 C  273  VAL THR LYS LEU VAL ALA ASN LEU PRO LYS ASP TYR MSE
SEQRES   5 C  273  ILE THR LEU LYS TYR VAL PRO GLY MSE ASP VAL LEU PRO
SEQRES   6 C  273  SER HIS CYS TRP ILE SER GLU MSE VAL VAL GLN LEU SER
SEQRES   7 C  273  ASP SER LEU THR ASP LEU LEU ASP LYS PHE SER ASN ILE
SEQRES   8 C  273  SER GLU GLY LEU SER ASN TYR SER ILE ILE ASP LYS LEU
SEQRES   9 C  273  VAL ASN ILE VAL ASP ASP LEU VAL GLU CYS VAL LYS GLU
SEQRES  10 C  273  ASN SER SER LYS ASP LEU LYS LYS SER PHE LYS SER PRO
SEQRES  11 C  273  GLU PRO ARG LEU PHE THR PRO GLU GLU PHE PHE ARG ILE
SEQRES  12 C  273  PHE ASN ARG SER ILE ASP ALA PHE LYS ASP PHE VAL VAL
SEQRES  13 C  273  ALA SER GLU THR SER ASP CYS VAL VAL SER SER THR LEU
SEQRES  14 C  273  SER PRO GLU LYS ASP SER ARG VAL SER VAL THR LYS PRO
SEQRES  15 C  273  PHE MET LEU PRO PRO VAL ALA ALA SER SER LEU ARG ASN
SEQRES  16 C  273  ASP SER SER SER SER ASN ARG LYS ALA LYS ASN PRO PRO
SEQRES  17 C  273  GLY ASP SER SER LEU HIS TRP ALA ALA MET ALA LEU PRO
SEQRES  18 C  273  ALA LEU PHE SER LEU ILE ILE GLY PHE ALA PHE GLY ALA
SEQRES  19 C  273  LEU TYR TRP LYS LYS ARG GLN PRO SER LEU THR ARG ALA
SEQRES  20 C  273  VAL GLU ASN ILE GLN ILE ASN GLU GLU ASP ASN GLU ILE
SEQRES  21 C  273  SER MET LEU GLN GLU LYS GLU ARG GLU PHE GLN GLU VAL
SEQRES   1 D  273  MET LYS LYS THR GLN THR TRP ILE LEU THR CYS ILE TYR
SEQRES   2 D  273  LEU GLN LEU LEU LEU PHE ASN PRO LEU VAL LYS THR GLU
SEQRES   3 D  273  GLY ILE CYS ARG ASN ARG VAL THR ASN ASN VAL LYS ASP
SEQRES   4 D  273  VAL THR LYS LEU VAL ALA ASN LEU PRO LYS ASP TYR MSE
SEQRES   5 D  273  ILE THR LEU LYS TYR VAL PRO GLY MSE ASP VAL LEU PRO
SEQRES   6 D  273  SER HIS CYS TRP ILE SER GLU MSE VAL VAL GLN LEU SER
SEQRES   7 D  273  ASP SER LEU THR ASP LEU LEU ASP LYS PHE SER ASN ILE
SEQRES   8 D  273  SER GLU GLY LEU SER ASN TYR SER ILE ILE ASP LYS LEU
SEQRES   9 D  273  VAL ASN ILE VAL ASP ASP LEU VAL GLU CYS VAL LYS GLU
SEQRES  10 D  273  ASN SER SER LYS ASP LEU LYS LYS SER PHE LYS SER PRO
SEQRES  11 D  273  GLU PRO ARG LEU PHE THR PRO GLU GLU PHE PHE ARG ILE
SEQRES  12 D  273  PHE ASN ARG SER ILE ASP ALA PHE LYS ASP PHE VAL VAL
SEQRES  13 D  273  ALA SER GLU THR SER ASP CYS VAL VAL SER SER THR LEU
SEQRES  14 D  273  SER PRO GLU LYS ASP SER ARG VAL SER VAL THR LYS PRO
SEQRES  15 D  273  PHE MET LEU PRO PRO VAL ALA ALA SER SER LEU ARG ASN
SEQRES  16 D  273  ASP SER SER SER SER ASN ARG LYS ALA LYS ASN PRO PRO
SEQRES  17 D  273  GLY ASP SER SER LEU HIS TRP ALA ALA MET ALA LEU PRO
SEQRES  18 D  273  ALA LEU PHE SER LEU ILE ILE GLY PHE ALA PHE GLY ALA
SEQRES  19 D  273  LEU TYR TRP LYS LYS ARG GLN PRO SER LEU THR ARG ALA
SEQRES  20 D  273  VAL GLU ASN ILE GLN ILE ASN GLU GLU ASP ASN GLU ILE
SEQRES  21 D  273  SER MET LEU GLN GLU LYS GLU ARG GLU PHE GLN GLU VAL
MODRES 1SCF MSE A   27  MET  SELENOMETHIONINE
MODRES 1SCF MSE A   36  MET  SELENOMETHIONINE
MODRES 1SCF MSE A   48  MET  SELENOMETHIONINE
MODRES 1SCF MSE B   27  MET  SELENOMETHIONINE
MODRES 1SCF MSE B   36  MET  SELENOMETHIONINE
MODRES 1SCF MSE B   48  MET  SELENOMETHIONINE
MODRES 1SCF MSE C   27  MET  SELENOMETHIONINE
MODRES 1SCF MSE C   36  MET  SELENOMETHIONINE
MODRES 1SCF MSE C   48  MET  SELENOMETHIONINE
MODRES 1SCF MSE D   27  MET  SELENOMETHIONINE
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Figure 8-9

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MODRES 1SCF MSE D   36  MET  SELENOMETHIONINE
MODRES 1SCF MSE D   48  MET  SELENOMETHIONINE
HET    MSE  A  27       8
HET    MSE  A  36       8
HET    MSE  A  48       8
HET    MSE  B  27       8
HET    MSE  B  36       8
HET    MSE  B  48       8
HET    MSE  C  27       8
HET    MSE  C  36       8
HET    MSE  C  48       8
HET    MSE  D  27       8
HET    MSE  D  36       8
HET    MSE  D  48       8
HET     CA   1021       1
HET     CA   1022       1
HET     CA   1023       1
HET    1PE      1      16
HETNAM     MSE SELENOMETHIONINE
HETNAM      CA CALCIUM ION
HETNAM     1PE POLYETHYLENE GLYCOL
HETSYN     1PE PEG400
FORMUL   1  MSE     3(C5 H11 N1 O2 SE1)
FORMUL   2  MSE     3(C5 H11 N1 O2 SE1)
FORMUL   3  MSE     3(C5 H11 N1 O2 SE1)
FORMUL   4  MSE     3(C5 H11 N1 O2 SE1)
FORMUL   5   CA     3(CA1 2+)
FORMUL   6  1PE     C10 H22 O6
FORMUL   7  HOH    *264(H2 O1)
HELIX    1   1 VAL A   12  ASN A   21  1                                   10
HELIX    2   2 SER A   41  CYS A   43  5                                    3
HELIX    3   3 SER A   46  LYS A   62  5                                   17
HELIX    4   4 ASN A   72  CYS A   89  1                                   18
HELIX    5   5 PRO A  112  LYS A  127  1                                   16
HELIX    6   6 VAL B   12  ASN B   21  1                                   10
HELIX    7   7 SER B   41  CYS B   43  5                                    3
HELIX    8   8 SER B   46  LYS B   62  5                                   17
HELIX    9   9 ASN B   72  GLU B   92  1                                   21
HELIX   10  10 PRO B  112  LYS B  127  1                                   16
HELIX   11  11 VAL C   12  ASN C   21  1                                   10
HELIX   12  12 SER C   41  LYS C   62  1                                   22
HELIX   13  13 ASN C   72  VAL C   90  1                                   19
HELIX   14  14 PRO C  112  ASP C  124  1                                   13
HELIX   15  15 VAL D   12  ASN D   21  1                                   10
HELIX   16  16 SER D   41  CYS D   43  5                                    3
HELIX   17  17 SER D   46  LYS D   62  5                                   17
HELIX   18  18 ASN D   72  CYS D   89  1                                   18
HELIX   19  19 PRO D  112  ALA D  125  1                                   14
SHEET    1   A 2 THR A  29  LYS A  31  0
SHEET    2   A 2 PRO A 107  LEU A 109 -1  N  ARG A 108   O  LEU A  30
SHEET    1   B 2 THR B  29  LYS B  31  0
SHEET    2   B 2 PRO B 107  LEU B 109 -1  N  ARG B 108   O  LEU B  30
SHEET    1   C 2 THR C  29  LYS C  31  0
SHEET    2   C 2 PRO C 107  LEU C 109 -1  N  ARG C 108   O  LEU C  30
SHEET    1   D 2 THR D  29  LYS D  31  0
SHEET    2   D 2 PRO D 107  LEU D 109 -1  N  ARG D 108   O  LEU D  30
SSBOND   1 CYS A   43    CYS A  138
SSBOND   2 CYS B   43    CYS B  138
LINK         N   MSE A  27                 C   TYR A  26
LINK         C   MSE A  27                 N   ILE A  28
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Figure 8-10

```
LINK         N   MSE A  36                 C   GLY A  35
LINK         C   MSE A  36                 N   ASP A  37
LINK         N   MSE A  48                 C   GLU A  47
LINK         C   MSE A  48                 N   VAL A  49
LINK         N   MSE B  27                 C   TYR B  26
LINK         C   MSE B  27                 N   ILE B  28
LINK         N   MSE B  36                 C   GLY B  35
LINK         C   MSE B  36                 N   ASP B  37
LINK         N   MSE B  48                 C   GLU B  47
LINK         C   MSE B  48                 N   VAL B  49
LINK         N   MSE C  27                 C   TYR C  26
LINK         C   MSE C  27                 N   ILE C  28
LINK         N   MSE C  36                 C   GLY C  35
LINK         C   MSE C  36                 N   ASP C  37
LINK         N   MSE C  48                 C   GLU C  47
LINK         C   MSE C  48                 N   VAL C  49
LINK         N   MSE D  27                 C   TYR D  26
LINK         C   MSE D  27                 N   ILE D  28
LINK         N   MSE D  36                 C   GLY D  35
LINK         C   MSE D  36                 N   ASP D  37
LINK         N   MSE D  48                 C   GLU D  47
LINK         C   MSE D  48                 N   VAL D  49
LINK        CA    CA 1021                 O   HOH  1024
LINK        CA    CA 1021                 O   HOH  1025
LINK        CA    CA 1023                 O   HOH  1027
LINK        CA    CA 1023                 O   HOH  1028
LINK        CA    CA 1023                 O   HOH  1029
CISPEP   1 SER A  104     PRO A  105          0        -0.10
CRYST1   71.820   82.550   88.190  90.00  90.00  90.00 P 21 21 21    4
ORIGX1      1.000000  0.000000  0.000000        0.00000
ORIGX2      0.000000  1.000000  0.000000        0.00000
ORIGX3      0.000000  0.000000  1.000000        0.00000
SCALE1      0.013924  0.000000  0.000000        0.00000
SCALE2      0.000000  0.012114  0.000000        0.00000
SCALE3      0.000000  0.000000  0.011339        0.00000
MTRIX1   1  0.915300  0.368400  0.162800      -10.34380    1
MTRIX2   1  0.357100 -0.929200  0.095000       35.55670    1
MTRIX3   1  0.186300 -0.028800 -0.982100       43.17570    1
MTRIX1   2 -0.935658 -0.315827 -0.157471       63.79985    1
MTRIX2   2 -0.265278  0.923709 -0.276386       17.94411    1
MTRIX3   2  0.232747 -0.216829 -0.948058       63.68074    1
MTRIX1   3 -0.994700  0.088300 -0.051700       54.54720    1
MTRIX2   3 -0.094000 -0.988400  0.119100       48.88150    1
MTRIX3   3 -0.040600  0.123400  0.991500      -20.54390    1
MTRIX1   4 -0.991100  0.100500 -0.087800       55.16840    1
MTRIX2   4 -0.117800 -0.968000  0.221700       45.07210    1
MTRIX3   4 -0.062700  0.230100  0.971100      -21.92400    1
MTRIX1   5 -0.951900 -0.248300  0.179700       52.26270    1
MTRIX2   5 -0.277100  0.947600 -0.158800       13.33780    1
MTRIX3   5 -0.130900 -0.200900 -0.970800       74.41510    1
MTRIX1   6  0.984200  0.147100 -0.098100        0.55340    1
MTRIX2   6  0.142600 -0.988400 -0.052100       52.60730    1
MTRIX3   6 -0.104600  0.037300 -0.993800       86.74100    1
MTRIX1   7 -0.955400 -0.244200  0.166100       52.84290    1
MTRIX2   7 -0.269500  0.950900 -0.152200       12.52990    1
MTRIX3   7 -0.120800 -0.190100 -0.974300       73.76110    1
ATOM     1  N   ASN A  11      10.232   3.110  20.636  1.00 60.07           N
ATOM     2  CA  ASN A  11       9.176   3.892  19.994  1.00 59.79           C
ATOM     3  C   ASN A  11       9.647   5.204  19.309  1.00 59.52           C
ATOM     4  O   ASN A  11       9.661   6.288  19.910  1.00 59.97           O
```

Figure 8-11

```
ATOM      5  CB  ASN A  11       8.113   4.228  21.038  1.00 60.46           C
ATOM      6  N   VAL A  12      10.013   5.143  18.009  1.00 57.40           N
ATOM      7  CA  VAL A  12      10.715   6.225  17.309  1.00 53.71           C
ATOM      8  C   VAL A  12       9.844   7.387  16.820  1.00 50.84           C
ATOM      9  O   VAL A  12      10.343   8.268  16.130  1.00 51.46           O
ATOM     10  CB  VAL A  12      11.541   5.657  16.126  1.00 53.25           C
ATOM     11  N   LYS A  13       8.543   7.490  17.147  1.00 49.07           N
ATOM     12  CA  LYS A  13       7.721   8.640  16.756  1.00 44.35           C
ATOM     13  C   LYS A  13       8.114   9.879  17.542  1.00 42.88           C
ATOM     14  O   LYS A  13       8.271  10.995  17.007  1.00 41.79           O
ATOM     15  CB  LYS A  13       6.258   8.378  17.093  1.00 44.76           C
ATOM     16  N   ASP A  14       8.283   9.557  18.839  1.00 38.29           N
ATOM     17  CA  ASP A  14       8.609  10.545  19.818  1.00 35.56           C
ATOM     18  C   ASP A  14      10.068  10.894  19.718  1.00 32.01           C
ATOM     19  O   ASP A  14      10.389  12.060  19.896  1.00 30.80           O
ATOM     20  CB  ASP A  14       8.151  10.072  21.200  1.00 38.77           C
ATOM     21  CG  ASP A  14       6.725  10.518  21.630  1.00 43.77           C
ATOM     22  OD1 ASP A  14       6.046  11.324  20.969  1.00 45.53           O
ATOM     23  OD2 ASP A  14       6.269  10.057  22.680  1.00 47.33           O
ATOM     24  N   VAL A  15      10.939   9.938  19.360  1.00 28.31           N
ATOM     25  CA  VAL A  15      12.335  10.224  19.089  1.00 27.35           C
ATOM     26  C   VAL A  15      12.510  11.219  17.959  1.00 29.06           C
ATOM     27  O   VAL A  15      13.265  12.166  18.138  1.00 32.49           O
ATOM     28  CB  VAL A  15      13.191   8.976  18.792  1.00 26.33           C
ATOM     29  CG1 VAL A  15      14.623   9.347  18.405  1.00 20.32           C
ATOM     30  CG2 VAL A  15      13.215   8.064  20.008  1.00 24.37           C
ATOM     31  N   THR A  16      11.858  11.085  16.807  1.00 28.42           N
ATOM     32  CA  THR A  16      11.968  12.085  15.758  1.00 27.97           C
ATOM     33  C   THR A  16      11.386  13.413  16.208  1.00 25.43           C
ATOM     34  O   THR A  16      12.020  14.418  15.905  1.00 25.82           O
ATOM     35  CB  THR A  16      11.357  11.646  14.385  1.00 27.70           C
ATOM     36  OG1 THR A  16       9.959  11.529  14.588  1.00 32.27           O
ATOM     37  CG2 THR A  16      11.931  10.335  13.912  1.00 25.71           C
ATOM     38  N   LYS A  17      10.243  13.459  16.928  1.00 24.83           N
ATOM     39  CA  LYS A  17       9.701  14.698  17.482  1.00 23.60           C
ATOM     40  C   LYS A  17      10.659  15.401  18.410  1.00 21.54           C
ATOM     41  O   LYS A  17      10.756  16.624  18.373  1.00 23.88           O
ATOM     42  CB  LYS A  17       8.365  14.488  18.206  1.00 27.08           C
ATOM     43  CG  LYS A  17       7.291  14.120  17.198  1.00 34.84           C
ATOM     44  CD  LYS A  17       5.881  14.040  17.781  1.00 40.64           C
ATOM     45  CE  LYS A  17       4.800  13.911  16.665  1.00 45.98           C
ATOM     46  NZ  LYS A  17       4.607  12.559  16.140  1.00 48.58           N
ATOM     47  N   LEU A  18      11.417  14.646  19.212  1.00 19.73           N
ATOM     48  CA  LEU A  18      12.377  15.207  20.151  1.00 17.98           C
ATOM     49  C   LEU A  18      13.544  15.778  19.401  1.00 17.55           C
ATOM     50  O   LEU A  18      13.813  16.959  19.523  1.00 17.68           O
ATOM     51  CB  LEU A  18      12.875  14.144  21.121  1.00 17.63           C
ATOM     52  CG  LEU A  18      13.850  14.582  22.216  1.00 15.34           C
ATOM     53  CD1 LEU A  18      13.278  15.668  23.080  1.00 15.28           C
ATOM     54  CD2 LEU A  18      14.253  13.389  23.032  1.00 14.40           C
ATOM     55  N   VAL A  19      14.189  14.952  18.577  1.00 18.35           N
ATOM     56  CA  VAL A  19      15.187  15.421  17.628  1.00 19.40           C
ATOM     57  C   VAL A  19      14.757  16.628  16.824  1.00 18.97           C
ATOM     58  O   VAL A  19      15.533  17.562  16.711  1.00 22.36           O
ATOM     59  CB  VAL A  19      15.668  14.325  16.729  1.00 18.19           C
ATOM     60  CG1 VAL A  19      16.675  14.817  15.708  1.00 20.68           C
ATOM     61  CG2 VAL A  19      16.422  13.390  17.612  1.00 19.91           C
ATOM     62  N   ALA A  20      13.530  16.732  16.366  1.00 18.27           N
ATOM     63  CA  ALA A  20      13.105  17.946  15.719  1.00 17.82           C
ATOM     64  C   ALA A  20      12.923  19.074  16.711  1.00 18.90           C
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Figure 8-12

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ATOM     65  O   ALA A  20      12.977  20.244  16.352  1.00 20.70           O
ATOM     66  CB  ALA A  20      11.777  17.661  15.059  1.00 17.70           C
ATOM     67  N   ASN A  21      12.677  18.787  17.979  1.00 20.04           N
ATOM     68  CA  ASN A  21      12.450  19.852  18.933  1.00 20.73           C
ATOM     69  C   ASN A  21      13.695  20.161  19.771  1.00 20.34           C
ATOM     70  O   ASN A  21      13.627  20.909  20.741  1.00 21.05           O
ATOM     71  CB  ASN A  21      11.235  19.456  19.751  1.00 20.84           C
ATOM     72  CG  ASN A  21      10.409  20.664  20.103  1.00 21.87           C
ATOM     73  OD1 ASN A  21      10.157  21.501  19.250  1.00 20.51           O
ATOM     74  ND2 ASN A  21       9.983  20.853  21.359  1.00 25.03           N
ATOM     75  N   LEU A  22      14.851  19.615  19.399  1.00 18.22           N
ATOM     76  CA  LEU A  22      16.129  19.924  20.000  1.00 17.27           C
ATOM     77  C   LEU A  22      17.023  20.733  19.051  1.00 19.37           C
ATOM     78  O   LEU A  22      17.001  20.468  17.851  1.00 19.69           O
ATOM     79  CB  LEU A  22      16.856  18.631  20.432  1.00 16.17           C
ATOM     80  CG  LEU A  22      16.342  17.790  21.598  1.00 14.77           C
ATOM     81  CD1 LEU A  22      17.058  16.447  21.768  1.00 14.07           C
ATOM     82  CD2 LEU A  22      16.463  18.606  22.862  1.00 11.82           C
ATOM     83  N   PRO A  23      17.833  21.728  19.457  1.00 19.42           N
ATOM     84  CA  PRO A  23      18.655  22.511  18.537  1.00 19.17           C
ATOM     85  C   PRO A  23      19.694  21.621  17.878  1.00 20.53           C
ATOM     86  O   PRO A  23      20.318  20.832  18.575  1.00 21.23           O
ATOM     87  CB  PRO A  23      19.341  23.488  19.459  1.00 18.21           C
ATOM     88  CG  PRO A  23      18.549  23.480  20.755  1.00 16.10           C
ATOM     89  CD  PRO A  23      18.206  22.015  20.846  1.00 17.73           C
ATOM     90  N   LYS A  24      19.959  21.716  16.571  1.00 23.65           N
ATOM     91  CA  LYS A  24      20.937  20.852  15.866  1.00 27.23           C
ATOM     92  C   LYS A  24      22.388  20.847  16.370  1.00 25.36           C
ATOM     93  O   LYS A  24      23.179  19.918  16.149  1.00 25.16           O
ATOM     94  CB  LYS A  24      20.931  21.150  14.332  1.00 29.02           C
ATOM     95  CG  LYS A  24      19.550  20.939  13.680  1.00 36.19           C
ATOM     96  CD  LYS A  24      19.557  21.512  12.245  1.00 43.22           C
ATOM     97  CE  LYS A  24      18.207  21.800  11.585  1.00 42.88           C
ATOM     98  NZ  LYS A  24      18.433  22.694  10.448  1.00 48.02           N
ATOM     99  N   ASP A  25      22.712  21.900  17.110  1.00 26.32           N
ATOM    100  CA  ASP A  25      24.060  22.087  17.653  1.00 28.70           C
ATOM    101  C   ASP A  25      24.209  22.024  19.180  1.00 26.91           C
ATOM    102  O   ASP A  25      25.225  22.386  19.785  1.00 27.43           O
ATOM    103  CB  ASP A  25      24.551  23.433  17.144  1.00 30.59           C
ATOM    104  CG  ASP A  25      23.780  24.615  17.684  1.00 33.09           C
ATOM    105  OD1 ASP A  25      22.556  24.529  17.847  1.00 34.74           O
ATOM    106  OD2 ASP A  25      24.421  25.638  17.933  1.00 37.53           O
ATOM    107  N   TYR A  26      23.122  21.605  19.808  1.00 24.09           N
ATOM    108  CA  TYR A  26      23.165  21.289  21.189  1.00 20.96           C
ATOM    109  C   TYR A  26      23.821  19.937  21.246  1.00 20.04           C
ATOM    110  O   TYR A  26      23.282  18.951  20.780  1.00 22.61           O
ATOM    111  CB  TYR A  26      21.759  21.239  21.710  1.00 20.00           C
ATOM    112  CG  TYR A  26      21.728  20.927  23.199  1.00 23.05           C
ATOM    113  CD1 TYR A  26      22.430  21.764  24.039  1.00 20.56           C
ATOM    114  CD2 TYR A  26      21.015  19.843  23.683  1.00 22.87           C
ATOM    115  CE1 TYR A  26      22.421  21.541  25.376  1.00 23.76           C
ATOM    116  CE2 TYR A  26      20.993  19.629  25.047  1.00 22.41           C
ATOM    117  CZ  TYR A  26      21.693  20.493  25.877  1.00 23.68           C
ATOM    118  OH  TYR A  26      21.661  20.353  27.259  1.00 22.67           O
HETATM  119  N   MSE A  27      25.003  19.890  21.809  1.00 21.07           N
HETATM  120  CA  MSE A  27      25.716  18.643  22.008  1.00 21.95           C
HETATM  121  C   MSE A  27      25.325  17.906  23.296  1.00 23.63           C
HETATM  122  O   MSE A  27      25.089  18.481  24.371  1.00 22.77           O
HETATM  123  CB  MSE A  27      27.201  18.955  22.055  1.00 27.32           C
HETATM  124  CG  MSE A  27      27.695  19.788  20.866  1.00 28.96           C
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Figure 8-13

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HETATM  125  SE   MSE A  27      27.207  18.877  19.234  1.00 37.24          SE
HETATM  126  CE   MSE A  27      28.489  17.511  19.371  1.00 26.83           C
ATOM    127  N    ILE A  28      25.250  16.576  23.165  1.00 22.91           N
ATOM    128  CA   ILE A  28      24.860  15.666  24.240  1.00 21.29           C
ATOM    129  C    ILE A  28      26.030  14.713  24.494  1.00 21.02           C
ATOM    130  O    ILE A  28      26.530  14.075  23.571  1.00 20.97           O
ATOM    131  CB   ILE A  28      23.550  14.901  23.870  1.00 19.78           C
ATOM    132  CG1  ILE A  28      22.372  15.818  23.534  1.00 17.37           C
ATOM    133  CG2  ILE A  28      23.147  14.006  25.006  1.00 18.93           C
ATOM    134  CD1  ILE A  28      21.207  15.120  22.805  1.00 16.08           C
ATOM    135  N    THR A  29      26.492  14.597  25.744  1.00 20.17           N
ATOM    136  CA   THR A  29      27.592  13.727  26.087  1.00 20.16           C
ATOM    137  C    THR A  29      27.065  12.315  26.319  1.00 20.21           C
ATOM    138  O    THR A  29      26.051  12.081  26.988  1.00 19.29           O
ATOM    139  CB   THR A  29      28.269  14.295  27.333  1.00 21.22           C
ATOM    140  OG1  THR A  29      28.515  15.655  27.048  1.00 24.08           O
ATOM    141  CG2  THR A  29      29.593  13.644  27.634  1.00 23.19           C
ATOM    142  N    LEU A  30      27.767  11.369  25.708  1.00 18.56           N
ATOM    143  CA   LEU A  30      27.462   9.976  25.862  1.00 17.76           C
ATOM    144  C    LEU A  30      28.824   9.351  25.959  1.00 18.41           C
ATOM    145  O    LEU A  30      29.738   9.774  25.283  1.00 20.72           O
ATOM    146  CB   LEU A  30      26.649   9.396  24.642  1.00 19.78           C
ATOM    147  CG   LEU A  30      26.350   7.884  24.473  1.00 14.53           C
ATOM    148  CD1  LEU A  30      25.475   7.478  25.601  1.00 18.04           C
ATOM    149  CD2  LEU A  30      25.629   7.525  23.205  1.00 14.92           C
ATOM    150  N    LYS A  31      28.984   8.379  26.833  1.00 18.64           N
ATOM    151  CA   LYS A  31      30.176   7.575  26.918  1.00 20.71           C
ATOM    152  C    LYS A  31      29.940   6.417  25.999  1.00 21.51           C
ATOM    153  O    LYS A  31      28.966   5.701  26.170  1.00 23.02           O
ATOM    154  CB   LYS A  31      30.411   7.009  28.295  1.00 19.63           C
ATOM    155  CG   LYS A  31      30.788   8.066  29.309  1.00 25.85           C
ATOM    156  CD   LYS A  31      31.154   7.355  30.605  1.00 29.83           C
ATOM    157  CE   LYS A  31      31.652   8.305  31.675  1.00 32.89           C
ATOM    158  NZ   LYS A  31      32.116   7.506  32.799  1.00 39.63           N
ATOM    159  N    TYR A  32      30.845   6.219  25.034  1.00 24.83           N
ATOM    160  CA   TYR A  32      30.565   5.424  23.844  1.00 22.31           C
ATOM    161  C    TYR A  32      31.607   4.359  23.767  1.00 19.55           C
ATOM    162  O    TYR A  32      32.759   4.667  23.946  1.00 22.18           O
ATOM    163  CB   TYR A  32      30.569   6.367  22.640  1.00 25.12           C
ATOM    164  CG   TYR A  32      30.557   5.725  21.262  1.00 27.46           C
ATOM    165  CD1  TYR A  32      31.790   5.449  20.689  1.00 26.41           C
ATOM    166  CD2  TYR A  32      29.369   5.437  20.613  1.00 26.10           C
ATOM    167  CE1  TYR A  32      31.871   4.860  19.452  1.00 27.56           C
ATOM    168  CE2  TYR A  32      29.462   4.854  19.356  1.00 29.60           C
ATOM    169  CZ   TYR A  32      30.710   4.589  18.787  1.00 28.41           C
ATOM    170  OH   TYR A  32      30.844   4.087  17.501  1.00 32.61           O
ATOM    171  N    VAL A  33      31.217   3.108  23.604  1.00 20.21           N
ATOM    172  CA   VAL A  33      32.138   2.022  23.453  1.00 22.23           C
ATOM    173  C    VAL A  33      32.829   2.212  22.110  1.00 24.20           C
ATOM    174  O    VAL A  33      32.156   2.231  21.078  1.00 24.76           O
ATOM    175  CB   VAL A  33      31.400   0.676  23.549  1.00 23.11           C
ATOM    176  CG1  VAL A  33      32.297  -0.537  23.309  1.00 22.36           C
ATOM    177  CG2  VAL A  33      30.857   0.535  24.951  1.00 25.26           C
ATOM    178  N    PRO A  34      34.158   2.380  22.078  1.00 25.19           N
ATOM    179  CA   PRO A  34      34.921   2.477  20.834  1.00 27.43           C
ATOM    180  C    PRO A  34      34.727   1.263  19.907  1.00 27.77           C
ATOM    181  O    PRO A  34      34.907   0.101  20.291  1.00 27.65           O
ATOM    182  CB   PRO A  34      36.381   2.586  21.335  1.00 29.54           C
ATOM    183  CG   PRO A  34      36.224   3.056  22.773  1.00 26.93           C
ATOM    184  CD   PRO A  34      35.043   2.269  23.245  1.00 23.54           C
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Figure 8-14

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ATOM    185  N   GLY A  35      34.312   1.550  18.666  1.00 28.92           N
ATOM    186  CA  GLY A  35      34.175   0.517  17.650  1.00 28.59           C
ATOM    187  C   GLY A  35      32.886  -0.277  17.715  1.00 28.76           C
ATOM    188  O   GLY A  35      32.743  -1.224  16.957  1.00 29.41           O
HETATM  189  N   MSE A  36      31.923   0.064  18.569  1.00 27.95           N
HETATM  190  CA  MSE A  36      30.612  -0.561  18.587  1.00 28.65           C
HETATM  191  C   MSE A  36      29.809  -0.477  17.276  1.00 28.45           C
HETATM  192  O   MSE A  36      28.824  -1.189  17.098  1.00 26.26           O
HETATM  193  CB  MSE A  36      29.774   0.036  19.739  1.00 32.71           C
HETATM  194  CG  MSE A  36      29.232   1.427  19.485  1.00 34.05           C
HETATM  195  SE  MSE A  36      27.946   2.252  20.676  1.00 36.59          SE
HETATM  196  CE  MSE A  36      26.309   1.728  19.841  1.00 26.94           C
ATOM    197  N   ASP A  37      30.212   0.393  16.338  1.00 30.42           N
ATOM    198  CA  ASP A  37      29.736   0.418  14.935  1.00 30.74           C
ATOM    199  C   ASP A  37      30.051  -0.794  14.038  1.00 27.32           C
ATOM    200  O   ASP A  37      29.344  -1.054  13.064  1.00 28.97           O
ATOM    201  CB  ASP A  37      30.200   1.716  14.234  1.00 33.15           C
ATOM    202  CG  ASP A  37      31.706   1.960  14.294  1.00 35.22           C
ATOM    203  OD1 ASP A  37      32.230   2.247  15.374  1.00 42.04           O
ATOM    204  OD2 ASP A  37      32.369   1.875  13.275  1.00 34.84           O
ATOM    205  N   VAL A  38      31.054  -1.584  14.381  1.00 23.11           N
ATOM    206  CA  VAL A  38      31.471  -2.713  13.566  1.00 23.69           C
ATOM    207  C   VAL A  38      31.568  -4.045  14.389  1.00 26.12           C
ATOM    208  O   VAL A  38      31.649  -5.172  13.882  1.00 27.25           O
ATOM    209  CB  VAL A  38      32.741  -2.089  12.936  1.00 19.85           C
ATOM    210  CG1 VAL A  38      34.023  -2.366  13.647  1.00 16.55           C
ATOM    211  CG2 VAL A  38      32.825  -2.379  11.512  1.00 19.54           C
ATOM    212  N   LEU A  39      31.464  -3.968  15.728  1.00 26.26           N
ATOM    213  CA  LEU A  39      31.505  -5.113  16.640  1.00 26.07           C
ATOM    214  C   LEU A  39      30.149  -5.788  16.888  1.00 25.48           C
ATOM    215  O   LEU A  39      29.130  -5.109  16.842  1.00 23.47           O
ATOM    216  CB  LEU A  39      32.061  -4.671  18.014  1.00 25.49           C
ATOM    217  CG  LEU A  39      33.515  -4.307  18.156  1.00 27.97           C
ATOM    218  CD1 LEU A  39      33.729  -3.645  19.510  1.00 30.79           C
ATOM    219  CD2 LEU A  39      34.399  -5.522  17.940  1.00 23.69           C
ATOM    220  N   PRO A  40      30.017  -7.086  17.192  1.00 25.65           N
ATOM    221  CA  PRO A  40      28.734  -7.665  17.563  1.00 27.77           C
ATOM    222  C   PRO A  40      28.061  -7.004  18.792  1.00 27.59           C
ATOM    223  O   PRO A  40      28.710  -6.411  19.658  1.00 26.55           O
ATOM    224  CB  PRO A  40      29.102  -9.122  17.683  1.00 27.41           C
ATOM    225  CG  PRO A  40      30.584  -9.150  18.015  1.00 26.93           C
ATOM    226  CD  PRO A  40      31.076  -8.082  17.099  1.00 26.35           C
ATOM    227  N   SER A  41      26.724  -7.026  18.830  1.00 27.40           N
ATOM    228  CA  SER A  41      26.003  -6.235  19.806  1.00 26.79           C
ATOM    229  C   SER A  41      26.288  -6.707  21.202  1.00 27.70           C
ATOM    230  O   SER A  41      26.451  -5.903  22.097  1.00 29.20           O
ATOM    231  CB  SER A  41      24.540  -6.240  19.558  1.00 23.46           C
ATOM    232  OG  SER A  41      24.074  -7.559  19.691  1.00 25.42           O
ATOM    233  N   HIS A  42      26.526  -8.007  21.355  1.00 29.95           N
ATOM    234  CA  HIS A  42      26.853  -8.594  22.636  1.00 30.32           C
ATOM    235  C   HIS A  42      28.076  -7.971  23.312  1.00 29.42           C
ATOM    236  O   HIS A  42      28.270  -8.138  24.524  1.00 28.56           O
ATOM    237  CB  HIS A  42      27.008 -10.109  22.451  1.00 35.10           C
ATOM    238  CG  HIS A  42      28.387 -10.616  21.997  1.00 39.36           C
ATOM    239  ND1 HIS A  42      29.424 -10.993  22.752  1.00 43.05           N
ATOM    240  CD2 HIS A  42      28.829 -10.644  20.694  1.00 42.30           C
ATOM    241  CE1 HIS A  42      30.472 -11.198  21.971  1.00 42.05           C
ATOM    242  NE2 HIS A  42      30.103 -10.969  20.735  1.00 41.31           N
ATOM    243  N   CYS A  43      28.888  -7.246  22.533  1.00 26.69           N
ATOM    244  CA  CYS A  43      30.112  -6.657  23.037  1.00 29.55           C
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Figure 8-15

```
ATOM    245  C   CYS A  43      29.916  -5.341  23.766  1.00 29.31           C
ATOM    246  O   CYS A  43      30.779  -4.912  24.512  1.00 31.36           O
ATOM    247  CB  CYS A  43      31.140  -6.395  21.915  1.00 31.15           C
ATOM    248  SG  CYS A  43      31.674  -7.929  21.120  1.00 35.60           S
ATOM    249  N   TRP A  44      28.813  -4.637  23.555  1.00 28.24           N
ATOM    250  CA  TRP A  44      28.704  -3.240  23.952  1.00 25.54           C
ATOM    251  C   TRP A  44      27.331  -2.947  24.498  1.00 25.35           C
ATOM    252  O   TRP A  44      27.173  -1.924  25.113  1.00 28.50           O
ATOM    253  CB  TRP A  44      28.965  -2.299  22.746  1.00 22.52           C
ATOM    254  CG  TRP A  44      28.207  -2.626  21.450  1.00 20.09           C
ATOM    255  CD1 TRP A  44      28.851  -3.316  20.455  1.00 19.03           C
ATOM    256  CD2 TRP A  44      26.890  -2.326  21.142  1.00 20.02           C
ATOM    257  NE1 TRP A  44      27.948  -3.464  19.527  1.00 20.48           N
ATOM    258  CE2 TRP A  44      26.791  -2.877  19.882  1.00 19.41           C
ATOM    259  CE3 TRP A  44      25.841  -1.609  21.652  1.00 18.83           C
ATOM    260  CZ2 TRP A  44      25.665  -2.678  19.127  1.00 16.33           C
ATOM    261  CZ3 TRP A  44      24.711  -1.431  20.910  1.00 16.81           C
ATOM    262  CH2 TRP A  44      24.617  -1.962  19.653  1.00 17.88           C
ATOM    263  N   ILE A  45      26.328  -3.786  24.275  1.00 27.39           N
ATOM    264  CA  ILE A  45      24.934  -3.500  24.540  1.00 28.48           C
ATOM    265  C   ILE A  45      24.666  -3.370  26.025  1.00 29.97           C
ATOM    266  O   ILE A  45      23.770  -2.622  26.389  1.00 31.30           O
ATOM    267  CB  ILE A  45      24.055  -4.601  23.904  1.00 28.39           C
ATOM    268  CG1 ILE A  45      22.603  -4.220  23.795  1.00 28.24           C
ATOM    269  CG2 ILE A  45      24.152  -5.926  24.668  1.00 28.54           C
ATOM    270  CD1 ILE A  45      22.371  -2.868  23.098  1.00 30.38           C
ATOM    271  N   SER A  46      25.408  -4.044  26.900  1.00 30.95           N
ATOM    272  CA  SER A  46      25.200  -3.897  28.337  1.00 32.47           C
ATOM    273  C   SER A  46      25.677  -2.546  28.844  1.00 30.61           C
ATOM    274  O   SER A  46      24.974  -1.880  29.597  1.00 30.88           O
ATOM    275  CB  SER A  46      25.899  -5.016  29.106  1.00 35.61           C
ATOM    276  OG  SER A  46      25.387  -6.311  28.746  1.00 43.59           O
ATOM    277  N   GLU A  47      26.840  -2.123  28.370  1.00 28.57           N
ATOM    278  CA  GLU A  47      27.355  -0.823  28.680  1.00 28.90           C
ATOM    279  C   GLU A  47      26.567   0.306  28.090  1.00 27.44           C
ATOM    280  O   GLU A  47      26.383   1.323  28.735  1.00 28.17           O
ATOM    281  CB  GLU A  47      28.791  -0.702  28.244  1.00 30.74           C
ATOM    282  CG  GLU A  47      29.439   0.554  28.818  1.00 34.60           C
ATOM    283  CD  GLU A  47      29.550   0.665  30.351  1.00 37.52           C
ATOM    284  OE1 GLU A  47      28.998  -0.153  31.107  1.00 37.54           O
ATOM    285  OE2 GLU A  47      30.208   1.607  30.800  1.00 38.33           O
HETATM  286  N   MSE A  48      26.073   0.098  26.879  1.00 27.89           N
HETATM  287  CA  MSE A  48      25.327   1.113  26.154  1.00 28.18           C
HETATM  288  C   MSE A  48      23.945   1.421  26.667  1.00 26.21           C
HETATM  289  O   MSE A  48      23.580   2.578  26.606  1.00 27.02           O
HETATM  290  CB  MSE A  48      25.309   0.882  24.637  1.00 29.23           C
HETATM  291  CG  MSE A  48      26.739   1.048  24.095  1.00 28.12           C
HETATM  292  SE  MSE A  48      27.685   2.655  24.690  1.00 35.61          SE
HETATM  293  CE  MSE A  48      26.476   3.857  23.743  1.00 22.58           C
ATOM    294  N   VAL A  49      23.147   0.491  27.195  1.00 27.65           N
ATOM    295  CA  VAL A  49      21.882   0.875  27.814  1.00 27.43           C
ATOM    296  C   VAL A  49      22.017   1.680  29.115  1.00 27.42           C
ATOM    297  O   VAL A  49      21.224   2.595  29.394  1.00 27.48           O
ATOM    298  CB  VAL A  49      20.884  -0.284  27.907  1.00 27.18           C
ATOM    299  CG1 VAL A  49      20.438  -0.478  26.452  1.00 27.08           C
ATOM    300  CG2 VAL A  49      21.421  -1.534  28.610  1.00 23.66           C
ATOM    301  N   VAL A  50      23.100   1.370  29.847  1.00 26.26           N
ATOM    302  CA  VAL A  50      23.469   2.060  31.068  1.00 24.75           C
ATOM    303  C   VAL A  50      23.964   3.431  30.716  1.00 25.57           C
ATOM    304  O   VAL A  50      23.485   4.384  31.320  1.00 28.77           O
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Figure 8-16

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ATOM    305  CB  VAL A  50      24.545   1.307  31.812  1.00 24.44           C
ATOM    306  CG1 VAL A  50      25.062   2.106  32.969  1.00 23.79           C
ATOM    307  CG2 VAL A  50      23.952   0.040  32.382  1.00 24.17           C
ATOM    308  N   GLN A  51      24.888   3.551  29.758  1.00 22.88           N
ATOM    309  CA  GLN A  51      25.315   4.841  29.294  1.00 18.59           C
ATOM    310  C   GLN A  51      24.226   5.698  28.700  1.00 18.17           C
ATOM    311  O   GLN A  51      24.223   6.904  28.948  1.00 20.05           O
ATOM    312  CB  GLN A  51      26.474   4.707  28.320  1.00 21.19           C
ATOM    313  CG  GLN A  51      27.676   4.059  28.934  1.00 17.37           C
ATOM    314  CD  GLN A  51      28.072   4.720  30.240  1.00 21.56           C
ATOM    315  OE1 GLN A  51      27.879   5.913  30.476  1.00 23.67           O
ATOM    316  NE2 GLN A  51      28.662   3.969  31.152  1.00 22.77           N
ATOM    317  N   LEU A  52      23.291   5.106  27.959  1.00 15.38           N
ATOM    318  CA  LEU A  52      22.210   5.850  27.374  1.00 16.72           C
ATOM    319  C   LEU A  52      21.199   6.284  28.411  1.00 18.34           C
ATOM    320  O   LEU A  52      20.676   7.387  28.382  1.00 18.73           O
ATOM    321  CB  LEU A  52      21.533   5.006  26.309  1.00 15.91           C
ATOM    322  CG  LEU A  52      22.207   5.059  24.928  1.00 17.11           C
ATOM    323  CD1 LEU A  52      21.807   3.849  24.155  1.00 14.42           C
ATOM    324  CD2 LEU A  52      21.886   6.330  24.184  1.00 12.26           C
ATOM    325  N   SER A  53      20.932   5.433  29.378  1.00 20.83           N
ATOM    326  CA  SER A  53      20.098   5.806  30.505  1.00 23.79           C
ATOM    327  C   SER A  53      20.716   6.966  31.295  1.00 24.20           C
ATOM    328  O   SER A  53      19.977   7.897  31.624  1.00 26.42           O
ATOM    329  CB  SER A  53      19.917   4.605  31.403  1.00 23.71           C
ATOM    330  OG  SER A  53      19.285   5.024  32.601  1.00 30.23           O
ATOM    331  N   ASP A  54      22.043   6.977  31.559  1.00 23.25           N
ATOM    332  CA  ASP A  54      22.687   8.036  32.308  1.00 20.61           C
ATOM    333  C   ASP A  54      22.659   9.325  31.572  1.00 19.02           C
ATOM    334  O   ASP A  54      22.303  10.358  32.142  1.00 20.41           O
ATOM    335  CB  ASP A  54      24.114   7.682  32.740  1.00 25.54           C
ATOM    336  CG  ASP A  54      24.207   6.579  33.815  1.00 31.33           C
ATOM    337  OD1 ASP A  54      23.185   5.965  34.178  1.00 36.02           O
ATOM    338  OD2 ASP A  54      25.318   6.318  34.307  1.00 32.62           O
ATOM    339  N   SER A  55      22.962   9.286  30.291  1.00 16.79           N
ATOM    340  CA  SER A  55      22.857  10.514  29.541  1.00 17.42           C
ATOM    341  C   SER A  55      21.454  11.096  29.425  1.00 16.81           C
ATOM    342  O   SER A  55      21.293  12.318  29.474  1.00 17.95           O
ATOM    343  CB  SER A  55      23.511  10.378  28.150  1.00 18.91           C
ATOM    344  OG  SER A  55      24.863   9.936  28.237  1.00 22.06           O
ATOM    345  N   LEU A  56      20.439  10.249  29.243  1.00 17.01           N
ATOM    346  CA  LEU A  56      19.073  10.726  29.162  1.00 17.99           C
ATOM    347  C   LEU A  56      18.518  11.188  30.514  1.00 18.27           C
ATOM    348  O   LEU A  56      17.800  12.186  30.575  1.00 18.82           O
ATOM    349  CB  LEU A  56      18.130   9.712  28.505  1.00 17.68           C
ATOM    350  CG  LEU A  56      18.061   9.584  26.983  1.00 18.44           C
ATOM    351  CD1 LEU A  56      17.381   8.280  26.613  1.00 19.03           C
ATOM    352  CD2 LEU A  56      17.392  10.764  26.321  1.00 16.39           C
ATOM    353  N   THR A  57      18.835  10.532  31.616  1.00 18.45           N
ATOM    354  CA  THR A  57      18.376  11.005  32.911  1.00 21.42           C
ATOM    355  C   THR A  57      18.975  12.383  33.205  1.00 21.42           C
ATOM    356  O   THR A  57      18.263  13.287  33.640  1.00 21.53           O
ATOM    357  CB  THR A  57      18.680   9.942  33.948  1.00 18.39           C
ATOM    358  OG1 THR A  57      18.055   8.791  33.418  1.00 20.01           O
ATOM    359  CG2 THR A  57      17.980  10.190  35.253  1.00 23.58           C
ATOM    360  N   ASP A  58      20.245  12.587  32.819  1.00 23.66           N
ATOM    361  CA  ASP A  58      20.908  13.867  32.971  1.00 24.99           C
ATOM    362  C   ASP A  58      20.269  14.969  32.162  1.00 23.11           C
ATOM    363  O   ASP A  58      20.243  16.133  32.567  1.00 22.89           O
ATOM    364  CB  ASP A  58      22.410  13.766  32.646  1.00 33.60           C
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Figure 8-17

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ATOM    365  CG  ASP A  58      23.101  15.151  32.595  1.00 41.66           C
ATOM    366  OD1 ASP A  58      23.500  15.636  33.666  1.00 45.37           O
ATOM    367  OD2 ASP A  58      23.204  15.764  31.502  1.00 43.30           O
ATOM    368  N   LEU A  59      19.762  14.614  30.994  1.00 21.38           N
ATOM    369  CA  LEU A  59      19.106  15.568  30.124  1.00 19.63           C
ATOM    370  C   LEU A  59      17.857  16.179  30.719  1.00 20.35           C
ATOM    371  O   LEU A  59      17.522  17.321  30.413  1.00 19.57           O
ATOM    372  CB  LEU A  59      18.751  14.826  28.859  1.00 19.31           C
ATOM    373  CG  LEU A  59      19.006  15.498  27.551  1.00 18.41           C
ATOM    374  CD1 LEU A  59      20.161  16.496  27.615  1.00 16.32           C
ATOM    375  CD2 LEU A  59      19.225  14.401  26.555  1.00 17.59           C
ATOM    376  N   LEU A  60      17.163  15.410  31.587  1.00 21.63           N
ATOM    377  CA  LEU A  60      15.930  15.857  32.216  1.00 20.55           C
ATOM    378  C   LEU A  60      16.133  17.147  32.974  1.00 22.32           C
ATOM    379  O   LEU A  60      15.264  18.016  32.929  1.00 23.28           O
ATOM    380  CB  LEU A  60      15.389  14.796  33.145  1.00 17.67           C
ATOM    381  CG  LEU A  60      14.680  13.601  32.538  1.00 14.57           C
ATOM    382  CD1 LEU A  60      14.293  12.641  33.643  1.00 12.83           C
ATOM    383  CD2 LEU A  60      13.462  14.048  31.847  1.00  8.22           C
ATOM    384  N   ASP A  61      17.338  17.285  33.558  1.00 22.42           N
ATOM    385  CA  ASP A  61      17.805  18.483  34.247  1.00 22.10           C
ATOM    386  C   ASP A  61      17.810  19.768  33.433  1.00 20.08           C
ATOM    387  O   ASP A  61      17.841  20.870  33.974  1.00 20.02           O
ATOM    388  CB  ASP A  61      19.203  18.169  34.753  1.00 28.60           C
ATOM    389  CG  ASP A  61      19.803  19.159  35.750  1.00 34.29           C
ATOM    390  OD1 ASP A  61      19.459  19.073  36.931  1.00 40.97           O
ATOM    391  OD2 ASP A  61      20.616  20.006  35.356  1.00 37.85           O
ATOM    392  N   LYS A  62      17.721  19.693  32.105  1.00 19.76           N
ATOM    393  CA  LYS A  62      17.839  20.862  31.245  1.00 16.53           C
ATOM    394  C   LYS A  62      16.485  21.335  30.770  1.00 16.75           C
ATOM    395  O   LYS A  62      16.388  22.383  30.130  1.00 17.62           O
ATOM    396  CB  LYS A  62      18.684  20.529  30.020  1.00 18.65           C
ATOM    397  CG  LYS A  62      19.986  19.755  30.233  1.00 16.80           C
ATOM    398  CD  LYS A  62      20.808  20.483  31.276  1.00 18.07           C
ATOM    399  CE  LYS A  62      22.135  19.776  31.535  1.00 23.34           C
ATOM    400  NZ  LYS A  62      22.088  18.331  31.330  1.00 28.06           N
ATOM    401  N   PHE A  63      15.400  20.605  31.068  1.00 16.40           N
ATOM    402  CA  PHE A  63      14.086  20.979  30.586  1.00 16.93           C
ATOM    403  C   PHE A  63      13.110  21.140  31.730  1.00 17.40           C
ATOM    404  O   PHE A  63      13.294  20.626  32.826  1.00 17.50           O
ATOM    405  CB  PHE A  63      13.576  19.942  29.574  1.00 15.08           C
ATOM    406  CG  PHE A  63      14.424  19.850  28.325  1.00 13.39           C
ATOM    407  CD1 PHE A  63      14.261  20.767  27.317  1.00 13.60           C
ATOM    408  CD2 PHE A  63      15.410  18.888  28.252  1.00 14.95           C
ATOM    409  CE1 PHE A  63      15.126  20.740  26.266  1.00 10.99           C
ATOM    410  CE2 PHE A  63      16.305  18.889  27.207  1.00 14.45           C
ATOM    411  CZ  PHE A  63      16.150  19.832  26.229  1.00 10.95           C
ATOM    412  N   SER A  64      12.031  21.843  31.444  1.00 19.14           N
ATOM    413  CA  SER A  64      10.993  22.080  32.407  1.00 21.71           C
ATOM    414  C   SER A  64       9.832  21.125  32.198  1.00 22.87           C
ATOM    415  O   SER A  64       9.431  20.758  31.098  1.00 24.09           O
ATOM    416  CB  SER A  64      10.533  23.508  32.261  1.00 22.47           C
ATOM    417  OG  SER A  64       9.408  23.881  33.049  1.00 29.46           O
ATOM    418  N   ASN A  65       9.298  20.809  33.363  1.00 23.97           N
ATOM    419  CA  ASN A  65       8.233  19.855  33.608  1.00 29.13           C
ATOM    420  C   ASN A  65       6.899  20.530  33.390  1.00 31.34           C
ATOM    421  O   ASN A  65       5.883  19.858  33.203  1.00 35.27           O
ATOM    422  CB  ASN A  65       8.309  19.551  35.119  1.00 30.43           C
ATOM    423  CG  ASN A  65       8.097  18.117  35.514  1.00 33.16           C
ATOM    424  OD1 ASN A  65       7.488  17.258  34.873  1.00 41.60           O
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Figure 8-18

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ATOM    425  ND2 ASN A  65       8.641  17.823  36.656  1.00 34.77           N
ATOM    426  N   ILE A  66       6.892  21.862  33.561  1.00 32.62           N
ATOM    427  CA  ILE A  66       5.708  22.691  33.384  1.00 33.83           C
ATOM    428  C   ILE A  66       5.681  23.071  31.918  1.00 35.58           C
ATOM    429  O   ILE A  66       6.450  23.910  31.431  1.00 36.08           O
ATOM    430  CB  ILE A  66       5.752  24.000  34.223  1.00 33.21           C
ATOM    431  CG1 ILE A  66       6.162  23.831  35.672  1.00 33.50           C
ATOM    432  CG2 ILE A  66       4.416  24.708  34.158  1.00 31.21           C
ATOM    433  CD1 ILE A  66       5.330  22.784  36.415  1.00 32.37           C
ATOM    434  N   SER A  67       4.782  22.424  31.201  1.00 37.23           N
ATOM    435  CA  SER A  67       4.669  22.650  29.771  1.00 40.50           C
ATOM    436  C   SER A  67       3.358  22.008  29.327  1.00 42.07           C
ATOM    437  O   SER A  67       3.073  20.841  29.622  1.00 43.86           O
ATOM    438  CB  SER A  67       5.892  21.985  29.075  1.00 40.62           C
ATOM    439  OG  SER A  67       6.244  22.539  27.815  1.00 36.76           O
ATOM    440  N   GLU A  68       2.502  22.765  28.648  1.00 44.40           N
ATOM    441  CA  GLU A  68       1.317  22.183  28.023  1.00 46.43           C
ATOM    442  C   GLU A  68       1.777  21.448  26.758  1.00 46.20           C
ATOM    443  O   GLU A  68       2.874  21.690  26.234  1.00 47.39           O
ATOM    444  CB  GLU A  68       0.364  23.301  27.637  1.00 49.01           C
ATOM    445  CG  GLU A  68      -1.051  22.858  27.256  1.00 53.42           C
ATOM    446  CD  GLU A  68      -2.066  23.229  28.324  1.00 56.12           C
ATOM    447  OE1 GLU A  68      -2.255  22.391  29.223  1.00 58.37           O
ATOM    448  OE2 GLU A  68      -2.634  24.342  28.250  1.00 56.09           O
ATOM    449  N   GLY A  69       0.957  20.523  26.262  1.00 45.44           N
ATOM    450  CA  GLY A  69       1.228  19.834  25.021  1.00 43.62           C
ATOM    451  C   GLY A  69       2.561  19.130  25.029  1.00 42.33           C
ATOM    452  O   GLY A  69       2.944  18.429  25.963  1.00 43.42           O
ATOM    453  N   LEU A  70       3.245  19.412  23.927  1.00 42.01           N
ATOM    454  CA  LEU A  70       4.567  18.856  23.634  1.00 40.66           C
ATOM    455  C   LEU A  70       5.570  19.283  24.688  1.00 37.48           C
ATOM    456  O   LEU A  70       5.769  20.477  24.916  1.00 39.56           O
ATOM    457  CB  LEU A  70       5.069  19.339  22.221  1.00 42.73           C
ATOM    458  CG  LEU A  70       6.365  18.753  21.553  1.00 43.68           C
ATOM    459  CD1 LEU A  70       6.429  17.212  21.539  1.00 40.99           C
ATOM    460  CD2 LEU A  70       6.506  19.318  20.134  1.00 42.81           C
ATOM    461  N   SER A  71       6.203  18.289  25.301  1.00 32.14           N
ATOM    462  CA  SER A  71       7.187  18.514  26.330  1.00 24.30           C
ATOM    463  C   SER A  71       8.394  17.653  26.032  1.00 20.06           C
ATOM    464  O   SER A  71       8.282  16.449  25.900  1.00 21.51           O
ATOM    465  CB  SER A  71       6.519  18.160  27.653  1.00 21.80           C
ATOM    466  OG  SER A  71       7.393  18.171  28.756  1.00 17.14           O
ATOM    467  N   ASN A  72       9.573  18.208  25.883  1.00 18.83           N
ATOM    468  CA  ASN A  72      10.787  17.419  25.827  1.00 16.99           C
ATOM    469  C   ASN A  72      11.079  16.692  27.083  1.00 15.54           C
ATOM    470  O   ASN A  72      11.566  15.578  26.997  1.00 16.64           O
ATOM    471  CB  ASN A  72      11.982  18.277  25.558  1.00 20.15           C
ATOM    472  CG  ASN A  72      11.916  18.839  24.158  1.00 23.44           C
ATOM    473  OD1 ASN A  72      11.109  18.421  23.317  1.00 25.67           O
ATOM    474  ND2 ASN A  72      12.780  19.812  23.894  1.00 24.59           N
ATOM    475  N   TYR A  73      10.823  17.309  28.239  1.00 15.06           N
ATOM    476  CA  TYR A  73      10.835  16.579  29.507  1.00 15.26           C
ATOM    477  C   TYR A  73       9.986  15.319  29.443  1.00 15.85           C
ATOM    478  O   TYR A  73      10.538  14.262  29.740  1.00 18.32           O
ATOM    479  CB  TYR A  73      10.315  17.410  30.733  1.00 12.75           C
ATOM    480  CG  TYR A  73      10.760  16.862  32.082  1.00 10.27           C
ATOM    481  CD1 TYR A  73      11.940  17.306  32.624  1.00 11.84           C
ATOM    482  CD2 TYR A  73       9.993  15.928  32.769  1.00 14.03           C
ATOM    483  CE1 TYR A  73      12.364  16.827  33.839  1.00 12.67           C
ATOM    484  CE2 TYR A  73      10.412  15.419  33.979  1.00 10.24           C
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Figure 8-19

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ATOM    485  CZ  TYR A  73      11.592  15.891  34.491  1.00 14.02           C
ATOM    486  OH  TYR A  73      12.042  15.429  35.703  1.00 14.54           O
ATOM    487  N   SER A  74       8.682  15.323  29.087  1.00 18.48           N
ATOM    488  CA  SER A  74       7.947  14.076  29.034  1.00 18.74           C
ATOM    489  C   SER A  74       8.429  13.074  28.017  1.00 18.80           C
ATOM    490  O   SER A  74       8.430  11.882  28.327  1.00 18.69           O
ATOM    491  CB  SER A  74       6.434  14.228  29.002  1.00 21.96           C
ATOM    492  OG  SER A  74       5.847  15.278  28.253  1.00 30.65           O
ATOM    493  N   ILE A  75       8.928  13.522  26.849  1.00 18.95           N
ATOM    494  CA  ILE A  75       9.481  12.602  25.855  1.00 17.82           C
ATOM    495  C   ILE A  75      10.689  11.896  26.422  1.00 17.12           C
ATOM    496  O   ILE A  75      10.679  10.688  26.557  1.00 18.03           O
ATOM    497  CB  ILE A  75       9.750  13.298  24.460  1.00 20.42           C
ATOM    498  CG1 ILE A  75       8.440  13.885  23.860  1.00 19.63           C
ATOM    499  CG2 ILE A  75      10.327  12.283  23.471  1.00 17.30           C
ATOM    500  CD1 ILE A  75       8.582  14.604  22.508  1.00 23.08           C
ATOM    501  N   ILE A  76      11.698  12.625  26.857  1.00 18.46           N
ATOM    502  CA  ILE A  76      12.916  12.070  27.436  1.00 19.33           C
ATOM    503  C   ILE A  76      12.622  11.116  28.592  1.00 19.01           C
ATOM    504  O   ILE A  76      13.199  10.040  28.714  1.00 20.65           O
ATOM    505  CB  ILE A  76      13.816  13.253  27.900  1.00 18.88           C
ATOM    506  CG1 ILE A  76      14.239  14.216  26.789  1.00 17.98           C
ATOM    507  CG2 ILE A  76      15.057  12.732  28.600  1.00 20.53           C
ATOM    508  CD1 ILE A  76      14.950  15.500  27.300  1.00 15.54           C
ATOM    509  N   ASP A  77      11.643  11.474  29.412  1.00 19.90           N
ATOM    510  CA  ASP A  77      11.226  10.682  30.562  1.00 19.93           C
ATOM    511  C   ASP A  77      10.627   9.341  30.177  1.00 21.32           C
ATOM    512  O   ASP A  77      10.832   8.318  30.830  1.00 21.41           O
ATOM    513  CB  ASP A  77      10.189  11.524  31.263  1.00 21.00           C
ATOM    514  CG  ASP A  77       9.506  10.808  32.390  1.00 23.32           C
ATOM    515  OD1 ASP A  77      10.211  10.249  33.204  1.00 26.02           O
ATOM    516  OD2 ASP A  77       8.283  10.750  32.419  1.00 24.74           O
ATOM    517  N   LYS A  78       9.835   9.312  29.101  1.00 23.41           N
ATOM    518  CA  LYS A  78       9.385   8.038  28.606  1.00 23.09           C
ATOM    519  C   LYS A  78      10.529   7.247  27.975  1.00 24.61           C
ATOM    520  O   LYS A  78      10.518   6.000  28.021  1.00 26.85           O
ATOM    521  CB  LYS A  78       8.267   8.237  27.656  1.00 25.84           C
ATOM    522  CG  LYS A  78       7.024   8.643  28.403  1.00 29.26           C
ATOM    523  CD  LYS A  78       5.882   8.766  27.362  1.00 40.97           C
ATOM    524  CE  LYS A  78       6.119   9.815  26.221  1.00 43.91           C
ATOM    525  NZ  LYS A  78       5.056   9.792  25.229  1.00 48.24           N
ATOM    526  N   LEU A  79      11.559   7.936  27.437  1.00 22.19           N
ATOM    527  CA  LEU A  79      12.718   7.253  26.865  1.00 18.09           C
ATOM    528  C   LEU A  79      13.577   6.757  27.968  1.00 16.82           C
ATOM    529  O   LEU A  79      14.146   5.692  27.806  1.00 17.74           O
ATOM    530  CB  LEU A  79      13.580   8.147  25.986  1.00 16.97           C
ATOM    531  CG  LEU A  79      12.928   8.748  24.768  1.00 15.98           C
ATOM    532  CD1 LEU A  79      13.984   9.540  24.058  1.00 16.93           C
ATOM    533  CD2 LEU A  79      12.264   7.721  23.857  1.00 14.76           C
ATOM    534  N   VAL A  80      13.609   7.460  29.101  1.00 16.48           N
ATOM    535  CA  VAL A  80      14.352   6.994  30.249  1.00 13.79           C
ATOM    536  C   VAL A  80      13.697   5.725  30.731  1.00 14.44           C
ATOM    537  O   VAL A  80      14.385   4.763  31.022  1.00 14.81           O
ATOM    538  CB  VAL A  80      14.382   8.054  31.331  1.00 17.12           C
ATOM    539  CG1 VAL A  80      14.937   7.490  32.631  1.00 17.65           C
ATOM    540  CG2 VAL A  80      15.307   9.189  30.910  1.00 13.43           C
ATOM    541  N   ASN A  81      12.383   5.633  30.743  1.00 16.27           N
ATOM    542  CA  ASN A  81      11.696   4.398  31.081  1.00 18.71           C
ATOM    543  C   ASN A  81      11.852   3.174  30.176  1.00 21.49           C
ATOM    544  O   ASN A  81      11.945   2.060  30.691  1.00 22.57           O
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Figure 8-20

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ATOM    545  CB  ASN A  81      10.244   4.707  31.191  1.00 20.64           C
ATOM    546  CG  ASN A  81       9.968   5.574  32.402  1.00 22.06           C
ATOM    547  OD1 ASN A  81      10.652   5.475  33.422  1.00 22.22           O
ATOM    548  ND2 ASN A  81       8.941   6.409  32.322  1.00 21.76           N
ATOM    549  N   ILE A  82      11.898   3.339  28.846  1.00 21.86           N
ATOM    550  CA  ILE A  82      12.226   2.270  27.917  1.00 23.02           C
ATOM    551  C   ILE A  82      13.602   1.742  28.112  1.00 23.67           C
ATOM    552  O   ILE A  82      13.728   0.536  28.067  1.00 26.85           O
ATOM    553  CB  ILE A  82      12.089   2.768  26.497  1.00 22.79           C
ATOM    554  CG1 ILE A  82      10.613   2.757  26.220  1.00 23.80           C
ATOM    555  CG2 ILE A  82      12.854   1.951  25.474  1.00 21.98           C
ATOM    556  CD1 ILE A  82      10.321   3.659  25.020  1.00 27.18           C
ATOM    557  N   VAL A  83      14.619   2.586  28.254  1.00 25.82           N
ATOM    558  CA  VAL A  83      15.996   2.104  28.338  1.00 27.82           C
ATOM    559  C   VAL A  83      16.212   1.471  29.706  1.00 30.01           C
ATOM    560  O   VAL A  83      16.995   0.522  29.796  1.00 32.08           O
ATOM    561  CB  VAL A  83      17.139   3.137  28.252  1.00 26.25           C
ATOM    562  CG1 VAL A  83      18.343   2.445  27.683  1.00 28.68           C
ATOM    563  CG2 VAL A  83      16.883   4.437  27.569  1.00 28.99           C
ATOM    564  N   ASP A  84      15.602   1.983  30.789  1.00 30.99           N
ATOM    565  CA  ASP A  84      15.711   1.384  32.123  1.00 34.08           C
ATOM    566  C   ASP A  84      15.125  -0.013  32.275  1.00 34.30           C
ATOM    567  O   ASP A  84      15.666  -0.816  33.035  1.00 35.01           O
ATOM    568  CB  ASP A  84      15.148   2.331  33.189  1.00 37.32           C
ATOM    569  CG  ASP A  84      15.909   3.664  33.316  1.00 42.03           C
ATOM    570  OD1 ASP A  84      16.907   3.865  32.621  1.00 43.39           O
ATOM    571  OD2 ASP A  84      15.496   4.523  34.107  1.00 44.86           O
ATOM    572  N   ASP A  85      14.055  -0.335  31.524  1.00 35.79           N
ATOM    573  CA  ASP A  85      13.554  -1.707  31.332  1.00 37.15           C
ATOM    574  C   ASP A  85      14.655  -2.665  30.860  1.00 34.71           C
ATOM    575  O   ASP A  85      14.777  -3.800  31.308  1.00 33.69           O
ATOM    576  CB  ASP A  85      12.434  -1.780  30.233  1.00 42.27           C
ATOM    577  CG  ASP A  85      11.023  -1.216  30.474  1.00 46.16           C
ATOM    578  OD1 ASP A  85      10.747  -0.756  31.587  1.00 46.14           O
ATOM    579  OD2 ASP A  85      10.197  -1.234  29.539  1.00 50.79           O
ATOM    580  N   LEU A  86      15.437  -2.164  29.904  1.00 33.83           N
ATOM    581  CA  LEU A  86      16.527  -2.886  29.288  1.00 33.71           C
ATOM    582  C   LEU A  86      17.747  -2.959  30.177  1.00 34.12           C
ATOM    583  O   LEU A  86      18.440  -3.965  30.083  1.00 34.86           O
ATOM    584  CB  LEU A  86      16.907  -2.260  27.948  1.00 31.87           C
ATOM    585  CG  LEU A  86      15.878  -2.198  26.829  1.00 30.75           C
ATOM    586  CD1 LEU A  86      16.383  -1.351  25.699  1.00 30.54           C
ATOM    587  CD2 LEU A  86      15.521  -3.581  26.349  1.00 29.51           C
ATOM    588  N   VAL A  87      18.033  -1.973  31.039  1.00 33.89           N
ATOM    589  CA  VAL A  87      19.121  -2.074  32.009  1.00 35.56           C
ATOM    590  C   VAL A  87      18.933  -3.223  33.039  1.00 40.73           C
ATOM    591  O   VAL A  87      19.889  -3.890  33.493  1.00 42.23           O
ATOM    592  CB  VAL A  87      19.239  -0.695  32.614  1.00 31.60           C
ATOM    593  CG1 VAL A  87      20.272  -0.634  33.703  1.00 33.57           C
ATOM    594  CG2 VAL A  87      19.680   0.253  31.537  1.00 29.91           C
ATOM    595  N   GLU A  88      17.645  -3.484  33.340  1.00 44.00           N
ATOM    596  CA  GLU A  88      17.191  -4.563  34.217  1.00 47.21           C
ATOM    597  C   GLU A  88      17.016  -5.918  33.542  1.00 48.21           C
ATOM    598  O   GLU A  88      17.359  -6.909  34.169  1.00 47.84           O
ATOM    599  CB  GLU A  88      15.868  -4.200  34.886  1.00 49.05           C
ATOM    600  CG  GLU A  88      15.877  -2.952  35.772  1.00 52.09           C
ATOM    601  CD  GLU A  88      16.809  -3.020  36.976  1.00 53.70           C
ATOM    602  OE1 GLU A  88      16.608  -3.858  37.861  1.00 55.01           O
ATOM    603  OE2 GLU A  88      17.744  -2.221  37.020  1.00 54.23           O
ATOM    604  N   CYS A  89      16.475  -6.018  32.311  1.00 50.79           N
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Figure 8-21

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ATOM    605  CA  CYS A  89      16.489  -7.244  31.503  1.00 54.51           C
ATOM    606  C   CYS A  89      17.952  -7.703  31.459  1.00 55.09           C
ATOM    607  O   CYS A  89      18.231  -8.791  31.961  1.00 57.42           O
ATOM    608  CB  CYS A  89      15.903  -6.972  30.078  1.00 57.17           C
ATOM    609  SG  CYS A  89      15.060  -8.280  29.096  1.00 64.80           S
ATOM    610  N   VAL A  90      18.890  -6.838  31.002  1.00 55.69           N
ATOM    611  CA  VAL A  90      20.357  -7.027  31.060  1.00 55.91           C
ATOM    612  C   VAL A  90      20.906  -7.397  32.450  1.00 57.84           C
ATOM    613  O   VAL A  90      22.014  -7.924  32.546  1.00 58.27           O
ATOM    614  CB  VAL A  90      21.074  -5.738  30.480  1.00 53.45           C
ATOM    615  CG1 VAL A  90      22.542  -5.564  30.824  1.00 52.76           C
ATOM    616  CG2 VAL A  90      20.965  -5.689  28.978  1.00 50.05           C
ATOM    617  N   LYS A  91      20.212  -7.128  33.558  1.00 59.29           N
ATOM    618  CA  LYS A  91      20.556  -7.785  34.810  1.00 62.11           C
ATOM    619  C   LYS A  91      19.865  -9.163  34.996  1.00 63.85           C
ATOM    620  O   LYS A  91      20.517 -10.061  35.533  1.00 66.48           O
ATOM    621  CB  LYS A  91      20.305  -6.837  35.993  1.00 61.39           C
ATOM    622  N   SER A 104      36.757   4.074  31.300  1.00 64.71           N
ATOM    623  CA  SER A 104      36.147   4.043  29.974  1.00 64.00           C
ATOM    624  C   SER A 104      34.723   3.416  29.904  1.00 61.57           C
ATOM    625  O   SER A 104      34.321   2.749  30.871  1.00 62.78           O
ATOM    626  CB  SER A 104      37.147   3.441  28.919  1.00 65.90           C
ATOM    627  OG  SER A 104      38.150   4.399  28.533  1.00 67.30           O
ATOM    628  N   PRO A 105      33.891   3.576  28.842  1.00 57.26           N
ATOM    629  CA  PRO A 105      34.173   4.332  27.635  1.00 53.19           C
ATOM    630  C   PRO A 105      34.452   5.801  27.827  1.00 51.76           C
ATOM    631  O   PRO A 105      34.107   6.397  28.848  1.00 53.30           O
ATOM    632  CB  PRO A 105      32.968   4.091  26.813  1.00 51.85           C
ATOM    633  CG  PRO A 105      31.869   3.765  27.755  1.00 53.45           C
ATOM    634  CD  PRO A 105      32.618   2.880  28.698  1.00 55.74           C
ATOM    635  N   GLU A 106      35.242   6.296  26.875  1.00 50.80           N
ATOM    636  CA  GLU A 106      35.584   7.700  26.790  1.00 47.97           C
ATOM    637  C   GLU A 106      34.332   8.435  26.350  1.00 44.14           C
ATOM    638  O   GLU A 106      33.684   8.006  25.400  1.00 42.91           O
ATOM    639  CB  GLU A 106      36.796   7.970  25.858  1.00 51.71           C
ATOM    640  CG  GLU A 106      36.873   7.196  24.509  1.00 57.13           C
ATOM    641  CD  GLU A 106      38.045   6.192  24.389  1.00 60.78           C
ATOM    642  OE1 GLU A 106      38.141   5.251  25.189  1.00 61.59           O
ATOM    643  OE2 GLU A 106      38.874   6.338  23.482  1.00 63.52           O
ATOM    644  N   PRO A 107      33.936   9.481  27.092  1.00 41.02           N
ATOM    645  CA  PRO A 107      32.846  10.386  26.770  1.00 38.74           C
ATOM    646  C   PRO A 107      33.069  11.190  25.517  1.00 37.93           C
ATOM    647  O   PRO A 107      34.148  11.749  25.271  1.00 40.00           O
ATOM    648  CB  PRO A 107      32.764  11.292  27.970  1.00 39.85           C
ATOM    649  CG  PRO A 107      34.162  11.290  28.542  1.00 40.91           C
ATOM    650  CD  PRO A 107      34.522   9.832  28.384  1.00 41.30           C
ATOM    651  N   ARG A 108      32.000  11.208  24.724  1.00 35.40           N
ATOM    652  CA  ARG A 108      32.006  11.864  23.436  1.00 33.34           C
ATOM    653  C   ARG A 108      30.766  12.722  23.318  1.00 29.75           C
ATOM    654  O   ARG A 108      29.727  12.347  23.867  1.00 29.55           O
ATOM    655  CB  ARG A 108      32.102  10.859  22.297  1.00 35.14           C
ATOM    656  CG  ARG A 108      33.480  10.219  22.313  1.00 39.55           C
ATOM    657  CD  ARG A 108      33.734   9.386  21.057  1.00 44.05           C
ATOM    658  NE  ARG A 108      34.715   8.324  21.284  1.00 45.36           N
ATOM    659  CZ  ARG A 108      34.965   7.376  20.373  1.00 45.18           C
ATOM    660  NH1 ARG A 108      34.481   7.446  19.142  1.00 46.89           N
ATOM    661  NH2 ARG A 108      35.679   6.306  20.712  1.00 46.89           N
ATOM    662  N   LEU A 109      30.932  13.877  22.650  1.00 26.42           N
ATOM    663  CA  LEU A 109      29.833  14.770  22.334  1.00 25.17           C
ATOM    664  C   LEU A 109      29.126  14.453  21.020  1.00 25.96           C
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Figure 8-22

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ATOM    665  O   LEU A 109      29.774  14.229  20.002  1.00 26.43           O
ATOM    666  CB  LEU A 109      30.316  16.182  22.280  1.00 24.30           C
ATOM    667  CG  LEU A 109      31.003  16.770  23.483  1.00 25.72           C
ATOM    668  CD1 LEU A 109      31.426  18.185  23.137  1.00 26.28           C
ATOM    669  CD2 LEU A 109      30.097  16.820  24.677  1.00 25.67           C
ATOM    670  N   PHE A 110      27.794  14.427  20.988  1.00 24.52           N
ATOM    671  CA  PHE A 110      27.019  14.004  19.822  1.00 22.36           C
ATOM    672  C   PHE A 110      25.996  15.079  19.586  1.00 21.47           C
ATOM    673  O   PHE A 110      25.618  15.777  20.525  1.00 21.05           O
ATOM    674  CB  PHE A 110      26.227  12.725  20.075  1.00 21.69           C
ATOM    675  CG  PHE A 110      27.133  11.561  20.318  1.00 23.01           C
ATOM    676  CD1 PHE A 110      27.676  10.892  19.238  1.00 24.43           C
ATOM    677  CD2 PHE A 110      27.506  11.243  21.597  1.00 21.68           C
ATOM    678  CE1 PHE A 110      28.614   9.897  19.463  1.00 24.92           C
ATOM    679  CE2 PHE A 110      28.460  10.282  21.798  1.00 22.08           C
ATOM    680  CZ  PHE A 110      29.017   9.597  20.746  1.00 23.51           C
ATOM    681  N   THR A 111      25.557  15.239  18.339  1.00 20.40           N
ATOM    682  CA  THR A 111      24.422  16.102  18.047  1.00 19.58           C
ATOM    683  C   THR A 111      23.175  15.367  18.473  1.00 15.81           C
ATOM    684  O   THR A 111      23.239  14.150  18.603  1.00 18.63           O
ATOM    685  CB  THR A 111      24.305  16.421  16.578  1.00 19.96           C
ATOM    686  OG1 THR A 111      24.145  15.178  15.907  1.00 21.91           O
ATOM    687  CG2 THR A 111      25.487  17.252  16.118  1.00 23.08           C
ATOM    688  N   PRO A 112      22.030  15.982  18.688  1.00 15.89           N
ATOM    689  CA  PRO A 112      20.783  15.254  18.984  1.00 16.41           C
ATOM    690  C   PRO A 112      20.500  14.089  18.025  1.00 17.10           C
ATOM    691  O   PRO A 112      20.329  12.954  18.431  1.00 18.32           O
ATOM    692  CB  PRO A 112      19.794  16.375  18.870  1.00 13.89           C
ATOM    693  CG  PRO A 112      20.581  17.559  19.386  1.00 14.36           C
ATOM    694  CD  PRO A 112      21.876  17.424  18.685  1.00 12.46           C
ATOM    695  N   GLU A 113      20.564  14.321  16.728  1.00 20.22           N
ATOM    696  CA  GLU A 113      20.393  13.303  15.737  1.00 24.11           C
ATOM    697  C   GLU A 113      21.371  12.143  15.864  1.00 24.55           C
ATOM    698  O   GLU A 113      20.963  10.982  15.866  1.00 25.38           O
ATOM    699  CB  GLU A 113      20.539  13.991  14.420  1.00 29.66           C
ATOM    700  CG  GLU A 113      20.432  13.029  13.250  1.00 41.26           C
ATOM    701  CD  GLU A 113      21.253  13.476  12.042  1.00 49.84           C
ATOM    702  OE1 GLU A 113      22.475  13.694  12.197  1.00 52.84           O
ATOM    703  OE2 GLU A 113      20.662  13.586  10.949  1.00 55.78           O
ATOM    704  N   GLU A 114      22.663  12.384  16.033  1.00 24.48           N
ATOM    705  CA  GLU A 114      23.594  11.291  16.198  1.00 22.26           C
ATOM    706  C   GLU A 114      23.398  10.486  17.471  1.00 22.80           C
ATOM    707  O   GLU A 114      23.564   9.256  17.494  1.00 23.87           O
ATOM    708  CB  GLU A 114      24.979  11.857  16.198  1.00 26.15           C
ATOM    709  CG  GLU A 114      25.362  12.534  14.897  1.00 32.62           C
ATOM    710  CD  GLU A 114      26.719  13.225  15.002  1.00 38.61           C
ATOM    711  OE1 GLU A 114      26.860  14.093  15.867  1.00 41.67           O
ATOM    712  OE2 GLU A 114      27.646  12.893  14.242  1.00 42.28           O
ATOM    713  N   PHE A 115      23.035  11.181  18.558  1.00 21.59           N
ATOM    714  CA  PHE A 115      22.812  10.544  19.850  1.00 19.30           C
ATOM    715  C   PHE A 115      21.601   9.645  19.667  1.00 17.06           C
ATOM    716  O   PHE A 115      21.555   8.527  20.165  1.00 17.46           O
ATOM    717  CB  PHE A 115      22.586  11.623  20.972  1.00 16.68           C
ATOM    718  CG  PHE A 115      22.148  11.018  22.298  1.00 13.67           C
ATOM    719  CD1 PHE A 115      20.820  10.679  22.520  1.00 15.42           C
ATOM    720  CD2 PHE A 115      23.081  10.752  23.261  1.00 15.56           C
ATOM    721  CE1 PHE A 115      20.412  10.003  23.650  1.00 16.48           C
ATOM    722  CE2 PHE A 115      22.674  10.136  24.429  1.00 17.36           C
ATOM    723  CZ  PHE A 115      21.351   9.750  24.617  1.00 18.29           C
ATOM    724  N   PHE A 116      20.581  10.135  18.981  1.00 18.67           N
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Figure 8-23

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ATOM    725  CA  PHE A 116      19.401   9.327  18.860  1.00 18.51           C
ATOM    726  C   PHE A 116      19.510   8.196  17.854  1.00 22.03           C
ATOM    727  O   PHE A 116      18.768   7.213  17.892  1.00 22.83           O
ATOM    728  CB  PHE A 116      18.204  10.195  18.687  1.00 19.13           C
ATOM    729  CG  PHE A 116      17.735  10.764  20.021  1.00 19.41           C
ATOM    730  CD1 PHE A 116      17.159   9.924  20.952  1.00 19.08           C
ATOM    731  CD2 PHE A 116      17.991  12.079  20.343  1.00 19.60           C
ATOM    732  CE1 PHE A 116      16.911  10.381  22.214  1.00 18.67           C
ATOM    733  CE2 PHE A 116      17.747  12.528  21.619  1.00 21.95           C
ATOM    734  CZ  PHE A 116      17.218  11.674  22.550  1.00 19.99           C
ATOM    735  N   ARG A 117      20.510   8.249  16.986  1.00 22.43           N
ATOM    736  CA  ARG A 117      20.822   7.134  16.123  1.00 21.98           C
ATOM    737  C   ARG A 117      21.453   6.076  16.971  1.00 19.70           C
ATOM    738  O   ARG A 117      21.039   4.946  16.841  1.00 22.56           O
ATOM    739  CB  ARG A 117      21.769   7.623  15.052  1.00 27.63           C
ATOM    740  CG  ARG A 117      22.329   6.596  14.082  1.00 36.33           C
ATOM    741  CD  ARG A 117      23.135   7.255  12.971  1.00 43.02           C
ATOM    742  NE  ARG A 117      22.296   8.207  12.239  1.00 49.61           N
ATOM    743  CZ  ARG A 117      22.704   9.468  12.008  1.00 54.02           C
ATOM    744  NH1 ARG A 117      23.915   9.867  12.474  1.00 53.58           N
ATOM    745  NH2 ARG A 117      21.899  10.314  11.313  1.00 53.56           N
ATOM    746  N   ILE A 118      22.394   6.348  17.874  1.00 19.56           N
ATOM    747  CA  ILE A 118      22.944   5.328  18.746  1.00 18.66           C
ATOM    748  C   ILE A 118      21.888   4.776  19.673  1.00 19.62           C
ATOM    749  O   ILE A 118      21.887   3.579  19.933  1.00 21.23           O
ATOM    750  CB  ILE A 118      24.054   5.970  19.533  1.00 21.60           C
ATOM    751  CG1 ILE A 118      25.121   6.479  18.593  1.00 22.63           C
ATOM    752  CG2 ILE A 118      24.665   5.002  20.534  1.00 22.20           C
ATOM    753  CD1 ILE A 118      26.178   7.330  19.285  1.00 23.90           C
ATOM    754  N   PHE A 119      20.971   5.619  20.180  1.00 20.06           N
ATOM    755  CA  PHE A 119      19.827   5.124  20.943  1.00 21.07           C
ATOM    756  C   PHE A 119      18.940   4.182  20.141  1.00 21.06           C
ATOM    757  O   PHE A 119      18.720   3.075  20.600  1.00 22.31           O
ATOM    758  CB  PHE A 119      19.001   6.253  21.590  1.00 18.55           C
ATOM    759  CG  PHE A 119      17.726   5.856  22.342  1.00 18.55           C
ATOM    760  CD1 PHE A 119      16.517   5.708  21.673  1.00 17.37           C
ATOM    761  CD2 PHE A 119      17.736   5.715  23.718  1.00 21.09           C
ATOM    762  CE1 PHE A 119      15.348   5.439  22.351  1.00 16.37           C
ATOM    763  CE2 PHE A 119      16.555   5.448  24.404  1.00 19.97           C
ATOM    764  CZ  PHE A 119      15.369   5.311  23.721  1.00 19.81           C
ATOM    765  N   ASN A 120      18.426   4.507  18.957  1.00 22.51           N
ATOM    766  CA  ASN A 120      17.567   3.577  18.222  1.00 23.92           C
ATOM    767  C   ASN A 120      18.284   2.316  17.841  1.00 25.82           C
ATOM    768  O   ASN A 120      17.653   1.274  17.841  1.00 26.73           O
ATOM    769  CB  ASN A 120      16.912   4.179  16.996  1.00 20.96           C
ATOM    770  CG  ASN A 120      15.857   5.195  17.377  1.00 24.90           C
ATOM    771  OD1 ASN A 120      14.852   4.877  18.020  1.00 30.44           O
ATOM    772  ND2 ASN A 120      16.044   6.458  17.023  1.00 26.09           N
ATOM    773  N   ARG A 121      19.605   2.390  17.632  1.00 29.29           N
ATOM    774  CA  ARG A 121      20.447   1.234  17.314  1.00 32.15           C
ATOM    775  C   ARG A 121      20.686   0.283  18.503  1.00 32.13           C
ATOM    776  O   ARG A 121      20.652  -0.949  18.369  1.00 32.27           O
ATOM    777  CB  ARG A 121      21.752   1.846  16.891  1.00 36.26           C
ATOM    778  CG  ARG A 121      22.606   0.988  16.001  1.00 42.80           C
ATOM    779  CD  ARG A 121      24.066   1.304  16.288  1.00 45.46           C
ATOM    780  NE  ARG A 121      24.730   0.026  16.469  1.00 49.59           N
ATOM    781  CZ  ARG A 121      25.603  -0.473  15.599  1.00 47.62           C
ATOM    782  NH1 ARG A 121      26.106   0.291  14.622  1.00 50.56           N
ATOM    783  NH2 ARG A 121      25.907  -1.764  15.692  1.00 41.39           N
ATOM    784  N   SER A 122      20.925   0.856  19.695  1.00 29.65           N
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Figure 8-24

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ATOM    785  CA  SER A 122      20.981   0.077  20.908  1.00 27.73           C
ATOM    786  C   SER A 122      19.643  -0.555  21.201  1.00 27.23           C
ATOM    787  O   SER A 122      19.603  -1.652  21.716  1.00 28.27           O
ATOM    788  CB  SER A 122      21.388   0.942  22.071  1.00 25.31           C
ATOM    789  OG  SER A 122      22.619   1.543  21.726  1.00 25.19           O
ATOM    790  N   ILE A 123      18.530   0.087  20.884  1.00 29.27           N
ATOM    791  CA  ILE A 123      17.210  -0.453  21.140  1.00 31.25           C
ATOM    792  C   ILE A 123      16.972  -1.618  20.207  1.00 32.43           C
ATOM    793  O   ILE A 123      16.522  -2.672  20.637  1.00 32.75           O
ATOM    794  CB  ILE A 123      16.129   0.661  20.973  1.00 33.20           C
ATOM    795  CG1 ILE A 123      16.103   1.685  22.130  1.00 35.29           C
ATOM    796  CG2 ILE A 123      14.739   0.181  20.629  1.00 33.87           C
ATOM    797  CD1 ILE A 123      16.243   1.313  23.627  1.00 32.91           C
ATOM    798  N   ASP A 124      17.325  -1.466  18.937  1.00 35.41           N
ATOM    799  CA  ASP A 124      17.064  -2.502  17.973  1.00 38.41           C
ATOM    800  C   ASP A 124      17.902  -3.728  18.170  1.00 38.55           C
ATOM    801  O   ASP A 124      17.386  -4.820  17.960  1.00 39.71           O
ATOM    802  CB  ASP A 124      17.074  -1.951  16.562  1.00 43.19           C
ATOM    803  CG  ASP A 124      15.763  -1.179  16.387  1.00 51.27           C
ATOM    804  OD1 ASP A 124      14.700  -1.790  16.620  1.00 56.07           O
ATOM    805  OD2 ASP A 124      15.784   0.020  16.039  1.00 54.65           O
ATOM    806  N   ALA A 125      19.102  -3.546  18.739  1.00 37.63           N
ATOM    807  CA  ALA A 125      20.039  -4.621  18.983  1.00 37.10           C
ATOM    808  C   ALA A 125      19.555  -5.682  19.944  1.00 39.02           C
ATOM    809  O   ALA A 125      20.250  -6.667  20.151  1.00 40.94           O
ATOM    810  CB  ALA A 125      21.321  -4.035  19.500  1.00 35.16           C
ATOM    811  N   PHE A 126      18.374  -5.538  20.549  1.00 41.54           N
ATOM    812  CA  PHE A 126      17.774  -6.599  21.363  1.00 45.13           C
ATOM    813  C   PHE A 126      16.837  -7.482  20.578  1.00 47.39           C
ATOM    814  O   PHE A 126      16.711  -8.660  20.900  1.00 48.19           O
ATOM    815  CB  PHE A 126      16.971  -6.099  22.571  1.00 45.19           C
ATOM    816  CG  PHE A 126      17.791  -5.456  23.683  1.00 44.53           C
ATOM    817  CD1 PHE A 126      18.239  -4.150  23.568  1.00 43.63           C
ATOM    818  CD2 PHE A 126      18.073  -6.184  24.815  1.00 44.69           C
ATOM    819  CE1 PHE A 126      18.960  -3.565  24.576  1.00 41.80           C
ATOM    820  CE2 PHE A 126      18.800  -5.597  25.822  1.00 43.70           C
ATOM    821  CZ  PHE A 126      19.238  -4.295  25.700  1.00 43.96           C
ATOM    822  N   LYS A 127      16.128  -6.898  19.600  1.00 50.61           N
ATOM    823  CA  LYS A 127      15.283  -7.656  18.679  1.00 53.56           C
ATOM    824  C   LYS A 127      16.149  -8.640  17.856  1.00 55.43           C
ATOM    825  O   LYS A 127      16.038  -9.876  17.922  1.00 57.14           O
ATOM    826  CB  LYS A 127      14.546  -6.638  17.764  1.00 51.56           C
ATOM    827  N   ASP A 128      17.077  -8.036  17.105  1.00 57.96           N
ATOM    828  CA  ASP A 128      18.105  -8.734  16.356  1.00 59.25           C
ATOM    829  C   ASP A 128      19.292  -9.249  17.190  1.00 59.16           C
ATOM    830  O   ASP A 128      20.461  -8.894  17.008  1.00 58.89           O
ATOM    831  CB  ASP A 128      18.492  -7.915  15.062  1.00 61.00           C
ATOM    832  CG  ASP A 128      18.868  -6.421  15.036  1.00 61.70           C
ATOM    833  OD1 ASP A 128      20.024  -6.078  15.330  1.00 63.63           O
ATOM    834  OD2 ASP A 128      18.015  -5.603  14.667  1.00 61.66           O
ATOM    835  N   PHE A 129      18.967 -10.151  18.118  1.00 59.49           N
ATOM    836  CA  PHE A 129      19.969 -10.719  19.002  1.00 61.20           C
ATOM    837  C   PHE A 129      20.411 -12.103  18.503  1.00 61.55           C
ATOM    838  O   PHE A 129      19.596 -12.979  18.179  1.00 61.67           O
ATOM    839  CB  PHE A 129      19.410 -10.801  20.440  1.00 64.40           C
ATOM    840  CG  PHE A 129      20.326 -10.282  21.561  1.00 67.62           C
ATOM    841  CD1 PHE A 129      21.642 -10.721  21.686  1.00 68.55           C
ATOM    842  CD2 PHE A 129      19.847  -9.338  22.473  1.00 69.51           C
ATOM    843  CE1 PHE A 129      22.464 -10.192  22.672  1.00 68.84           C
ATOM    844  CE2 PHE A 129      20.665  -8.823  23.472  1.00 68.79           C
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Figure 8-25

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ATOM    845  CZ  PHE A 129      21.976  -9.245  23.561  1.00 69.80           C
ATOM    846  N   VAL A 130      21.737 -12.294  18.417  1.00 60.68           N
ATOM    847  CA  VAL A 130      22.337 -13.577  18.041  1.00 60.72           C
ATOM    848  C   VAL A 130      23.459 -13.949  19.040  1.00 59.57           C
ATOM    849  O   VAL A 130      24.157 -13.076  19.597  1.00 58.08           O
ATOM    850  CB  VAL A 130      22.937 -13.560  16.582  1.00 60.98           C
ATOM    851  CG1 VAL A 130      23.051 -15.001  16.068  1.00 60.93           C
ATOM    852  CG2 VAL A 130      22.229 -12.635  15.579  1.00 58.32           C
ATOM    853  N   VAL A 131      23.635 -15.277  19.213  1.00 57.03           N
ATOM    854  CA  VAL A 131      24.634 -15.872  20.101  1.00 54.98           C
ATOM    855  C   VAL A 131      26.059 -15.336  19.950  1.00 53.17           C
ATOM    856  O   VAL A 131      26.547 -15.173  18.839  1.00 51.72           O
ATOM    857  CB  VAL A 131      24.563 -17.411  19.950  1.00 55.34           C
ATOM    858  CG1 VAL A 131      25.611 -18.162  20.780  1.00 55.30           C
ATOM    859  CG2 VAL A 131      23.145 -17.893  20.297  1.00 54.41           C
ATOM    860  N   ALA A 132      26.660 -15.027  21.117  1.00 52.91           N
ATOM    861  CA  ALA A 132      28.022 -14.512  21.293  1.00 52.69           C
ATOM    862  C   ALA A 132      29.161 -15.433  20.860  1.00 53.47           C
ATOM    863  O   ALA A 132      30.250 -15.019  20.445  1.00 52.96           O
ATOM    864  CB  ALA A 132      28.268 -14.176  22.771  1.00 48.84           C
ATOM    865  N   SER A 133      28.899 -16.725  21.000  1.00 55.81           N
ATOM    866  CA  SER A 133      29.812 -17.748  20.533  1.00 58.09           C
ATOM    867  C   SER A 133      29.744 -17.881  19.005  1.00 59.46           C
ATOM    868  O   SER A 133      30.726 -18.259  18.343  1.00 61.98           O
ATOM    869  CB  SER A 133      29.348 -19.047  21.161  1.00 59.31           C
ATOM    870  N   GLU A 134      28.556 -17.536  18.469  1.00 58.84           N
ATOM    871  CA  GLU A 134      28.251 -17.530  17.031  1.00 57.10           C
ATOM    872  C   GLU A 134      28.550 -16.218  16.298  1.00 54.08           C
ATOM    873  O   GLU A 134      28.319 -16.114  15.094  1.00 50.66           O
ATOM    874  CB  GLU A 134      26.768 -17.808  16.761  1.00 58.33           C
ATOM    875  CG  GLU A 134      26.269 -19.189  17.121  1.00 61.93           C
ATOM    876  CD  GLU A 134      24.955 -19.558  16.436  1.00 65.28           C
ATOM    877  OE1 GLU A 134      24.056 -18.711  16.294  1.00 64.83           O
ATOM    878  OE2 GLU A 134      24.853 -20.726  16.034  1.00 68.18           O
ATOM    879  N   THR A 135      28.999 -15.169  16.988  1.00 52.70           N
ATOM    880  CA  THR A 135      29.366 -13.953  16.291  1.00 51.61           C
ATOM    881  C   THR A 135      30.896 -13.856  16.192  1.00 51.35           C
ATOM    882  O   THR A 135      31.549 -14.721  15.580  1.00 52.93           O
ATOM    883  CB  THR A 135      28.621 -12.683  16.830  1.00 49.31           C
ATOM    884  OG1 THR A 135      29.039 -12.514  18.171  1.00 49.65           O
ATOM    885  CG2 THR A 135      27.108 -12.772  16.767  1.00 48.16           C
ATOM    886  N   SER A 136      31.473 -12.828  16.825  1.00 50.88           N
ATOM    887  CA  SER A 136      32.885 -12.502  16.714  1.00 49.48           C
ATOM    888  C   SER A 136      33.422 -12.163  18.121  1.00 47.44           C
ATOM    889  O   SER A 136      32.624 -12.000  19.056  1.00 46.14           O
ATOM    890  CB  SER A 136      32.966 -11.306  15.767  1.00 50.00           C
ATOM    891  OG  SER A 136      32.146 -11.504  14.615  1.00 52.41           O
ATOM    892  N   ASP A 137      34.760 -12.051  18.314  1.00 44.90           N
ATOM    893  CA  ASP A 137      35.366 -11.578  19.566  1.00 40.01           C
ATOM    894  C   ASP A 137      35.037 -10.093  19.850  1.00 36.45           C
ATOM    895  O   ASP A 137      34.105  -9.570  19.228  1.00 35.34           O
ATOM    896  CB  ASP A 137      36.879 -11.949  19.641  1.00 40.10           C
ATOM    897  CG  ASP A 137      37.915 -11.197  18.783  1.00 44.69           C
ATOM    898  OD1 ASP A 137      37.617 -10.121  18.252  1.00 46.41           O
ATOM    899  OD2 ASP A 137      39.056 -11.661  18.648  1.00 46.87           O
ATOM    900  N   CYS A 138      35.702  -9.337  20.741  1.00 32.95           N
ATOM    901  CA  CYS A 138      35.263  -7.982  21.014  1.00 31.28           C
ATOM    902  C   CYS A 138      36.311  -6.919  20.838  1.00 30.73           C
ATOM    903  O   CYS A 138      36.233  -5.825  21.414  1.00 31.32           O
ATOM    904  CB  CYS A 138      34.557  -7.854  22.361  1.00 32.08           C
```

Figure 8-26

```
ATOM    905  SG  CYS A 138      32.988  -8.777  22.463  1.00 37.40           S
ATOM    906  N   VAL A 139      37.258  -7.242  19.954  1.00 30.63           N
ATOM    907  CA  VAL A 139      38.333  -6.318  19.599  1.00 29.74           C
ATOM    908  C   VAL A 139      38.151  -5.898  18.168  1.00 28.81           C
ATOM    909  O   VAL A 139      37.830  -6.734  17.342  1.00 27.95           O
ATOM    910  CB  VAL A 139      39.769  -6.915  19.600  1.00 28.99           C
ATOM    911  CG1 VAL A 139      40.717  -5.884  20.195  1.00 29.64           C
ATOM    912  CG2 VAL A 139      39.889  -8.307  20.143  1.00 26.32           C
ATOM    913  N   VAL A 140      38.424  -4.646  17.840  1.00 31.00           N
ATOM    914  CA  VAL A 140      38.442  -4.247  16.459  1.00 34.50           C
ATOM    915  C   VAL A 140      39.899  -4.167  16.020  1.00 36.64           C
ATOM    916  O   VAL A 140      40.406  -5.059  15.323  1.00 39.48           O
ATOM    917  CB  VAL A 140      37.758  -2.914  16.217  1.00 36.55           C
ATOM    918  CG1 VAL A 140      37.417  -2.900  14.747  1.00 36.42           C
ATOM    919  CG2 VAL A 140      36.594  -2.569  17.119  1.00 34.81           C
ATOM    920  N   SER A 141      40.566  -3.136  16.529  1.00 37.83           N
ATOM    921  CA  SER A 141      41.905  -2.682  16.123  1.00 41.81           C
ATOM    922  C   SER A 141      41.936  -1.563  15.056  1.00 42.37           C
ATOM    923  O   SER A 141      43.035  -1.174  14.685  1.00 43.60           O
ATOM    924  CB  SER A 141      42.986  -3.811  15.889  1.00 42.08           C
ATOM    925  OG  SER A 141      43.175  -4.693  17.008  1.00 38.01           O
TER     927      SER A 141
ATOM    928  N   ASN B  11       2.666  37.382  21.946  1.00 65.93           N
ATOM    929  CA  ASN B  11       1.945  36.256  22.556  1.00 66.50           C
ATOM    930  C   ASN B  11       2.726  35.510  23.658  1.00 66.17           C
ATOM    931  O   ASN B  11       3.559  34.641  23.372  1.00 66.24           O
ATOM    932  CB  ASN B  11       1.488  35.204  21.515  1.00 66.50           C
ATOM    933  N   VAL B  12       2.404  35.814  24.934  1.00 65.43           N
ATOM    934  CA  VAL B  12       3.197  35.450  26.131  1.00 62.92           C
ATOM    935  C   VAL B  12       3.195  33.985  26.631  1.00 60.27           C
ATOM    936  O   VAL B  12       4.143  33.547  27.294  1.00 59.00           O
ATOM    937  CB  VAL B  12       2.780  36.430  27.299  1.00 64.35           C
ATOM    938  CG1 VAL B  12       1.408  36.086  27.935  1.00 63.94           C
ATOM    939  CG2 VAL B  12       3.908  36.621  28.318  1.00 63.41           C
ATOM    940  N   LYS B  13       2.125  33.208  26.374  1.00 56.82           N
ATOM    941  CA  LYS B  13       2.071  31.821  26.800  1.00 51.85           C
ATOM    942  C   LYS B  13       3.021  31.001  25.927  1.00 48.88           C
ATOM    943  O   LYS B  13       3.595  30.003  26.380  1.00 49.33           O
ATOM    944  CB  LYS B  13       0.640  31.283  26.675  1.00 52.25           C
ATOM    945  N   ASP B  14       3.258  31.456  24.684  1.00 44.12           N
ATOM    946  CA  ASP B  14       4.169  30.783  23.770  1.00 37.71           C
ATOM    947  C   ASP B  14       5.662  30.978  24.040  1.00 31.42           C
ATOM    948  O   ASP B  14       6.413  30.026  23.895  1.00 30.29           O
ATOM    949  CB  ASP B  14       3.763  31.113  22.326  1.00 40.87           C
ATOM    950  CG  ASP B  14       2.497  30.409  21.803  1.00 44.08           C
ATOM    951  OD1 ASP B  14       1.832  29.636  22.531  1.00 44.87           O
ATOM    952  OD2 ASP B  14       2.192  30.662  20.631  1.00 45.27           O
ATOM    953  N   VAL B  15       6.165  32.130  24.468  1.00 25.72           N
ATOM    954  CA  VAL B  15       7.545  32.234  24.906  1.00 24.93           C
ATOM    955  C   VAL B  15       7.872  31.357  26.112  1.00 26.84           C
ATOM    956  O   VAL B  15       8.935  30.739  26.124  1.00 29.81           O
ATOM    957  CB  VAL B  15       7.914  33.670  25.178  1.00 22.45           C
ATOM    958  CG1 VAL B  15       9.335  33.803  25.722  1.00 18.01           C
ATOM    959  CG2 VAL B  15       7.730  34.435  23.895  1.00 21.89           C
ATOM    960  N   THR B  16       6.962  31.275  27.104  1.00 27.60           N
ATOM    961  CA  THR B  16       7.040  30.393  28.276  1.00 28.70           C
ATOM    962  C   THR B  16       7.191  28.905  27.903  1.00 27.24           C
ATOM    963  O   THR B  16       8.063  28.227  28.442  1.00 29.07           O
ATOM    964  CB  THR B  16       5.797  30.649  29.237  1.00 30.92           C
ATOM    965  OG1 THR B  16       5.967  31.920  29.887  1.00 30.85           O
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Figure 8-27

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ATOM    966  CG2 THR B  16       5.605  29.577  30.304  1.00 29.47           C
ATOM    967  N   LYS B  17       6.385  28.387  26.979  1.00 24.02           N
ATOM    968  CA  LYS B  17       6.508  27.042  26.455  1.00 25.48           C
ATOM    969  C   LYS B  17       7.776  26.845  25.607  1.00 22.72           C
ATOM    970  O   LYS B  17       8.397  25.806  25.690  1.00 22.89           O
ATOM    971  CB  LYS B  17       5.235  26.851  25.662  1.00 29.47           C
ATOM    972  CG  LYS B  17       5.047  25.479  25.076  1.00 36.80           C
ATOM    973  CD  LYS B  17       3.820  25.460  24.129  1.00 40.47           C
ATOM    974  CE  LYS B  17       3.432  24.008  23.742  1.00 42.23           C
ATOM    975  NZ  LYS B  17       4.518  23.260  23.099  1.00 40.28           N
ATOM    976  N   LEU B  18       8.223  27.840  24.836  1.00 21.80           N
ATOM    977  CA  LEU B  18       9.489  27.797  24.148  1.00 19.84           C
ATOM    978  C   LEU B  18      10.608  27.757  25.151  1.00 19.53           C
ATOM    979  O   LEU B  18      11.425  26.868  24.985  1.00 22.71           O
ATOM    980  CB  LEU B  18       9.660  28.989  23.206  1.00 17.63           C
ATOM    981  CG  LEU B  18      10.954  29.148  22.479  1.00 13.25           C
ATOM    982  CD1 LEU B  18      11.216  27.956  21.627  1.00 16.15           C
ATOM    983  CD2 LEU B  18      10.895  30.338  21.606  1.00 13.19           C
ATOM    984  N   VAL B  19      10.670  28.606  26.187  1.00 17.49           N
ATOM    985  CA  VAL B  19      11.713  28.547  27.193  1.00 15.59           C
ATOM    986  C   VAL B  19      11.708  27.199  27.912  1.00 16.76           C
ATOM    987  O   VAL B  19      12.763  26.598  28.121  1.00 18.54           O
ATOM    988  CB  VAL B  19      11.587  29.741  28.170  1.00 15.79           C
ATOM    989  CG1 VAL B  19      12.566  29.662  29.308  1.00 13.19           C
ATOM    990  CG2 VAL B  19      11.922  31.014  27.489  1.00 12.62           C
ATOM    991  N   ALA B  20      10.533  26.655  28.232  1.00 17.26           N
ATOM    992  CA  ALA B  20      10.415  25.384  28.918  1.00 17.20           C
ATOM    993  C   ALA B  20      10.866  24.235  28.075  1.00 20.20           C
ATOM    994  O   ALA B  20      11.185  23.166  28.578  1.00 22.02           O
ATOM    995  CB  ALA B  20       8.972  25.064  29.185  1.00 18.25           C
ATOM    996  N   ASN B  21      10.854  24.390  26.763  1.00 22.32           N
ATOM    997  CA  ASN B  21      11.373  23.351  25.920  1.00 21.93           C
ATOM    998  C   ASN B  21      12.711  23.661  25.314  1.00 21.34           C
ATOM    999  O   ASN B  21      13.114  22.930  24.441  1.00 23.28           O
ATOM   1000  CB  ASN B  21      10.378  23.022  24.873  1.00 26.17           C
ATOM   1001  CG  ASN B  21       9.256  22.250  25.531  1.00 31.77           C
ATOM   1002  OD1 ASN B  21       9.352  21.054  25.813  1.00 30.41           O
ATOM   1003  ND2 ASN B  21       8.168  22.955  25.820  1.00 34.22           N
ATOM   1004  N   LEU B  22      13.455  24.675  25.727  1.00 20.84           N
ATOM   1005  CA  LEU B  22      14.825  24.880  25.285  1.00 18.95           C
ATOM   1006  C   LEU B  22      15.754  24.358  26.359  1.00 19.14           C
ATOM   1007  O   LEU B  22      15.428  24.560  27.526  1.00 19.71           O
ATOM   1008  CB  LEU B  22      15.097  26.380  25.022  1.00 17.41           C
ATOM   1009  CG  LEU B  22      14.510  27.035  23.750  1.00 15.79           C
ATOM   1010  CD1 LEU B  22      14.718  28.544  23.724  1.00 13.61           C
ATOM   1011  CD2 LEU B  22      15.120  26.381  22.517  1.00 14.80           C
ATOM   1012  N   PRO B  23      16.903  23.701  26.091  1.00 18.35           N
ATOM   1013  CA  PRO B  23      17.831  23.260  27.130  1.00 17.51           C
ATOM   1014  C   PRO B  23      18.329  24.418  28.008  1.00 17.87           C
ATOM   1015  O   PRO B  23      18.703  25.449  27.473  1.00 18.03           O
ATOM   1016  CB  PRO B  23      18.908  22.619  26.307  1.00 13.87           C
ATOM   1017  CG  PRO B  23      18.299  22.223  25.002  1.00 12.84           C
ATOM   1018  CD  PRO B  23      17.457  23.421  24.762  1.00 14.01           C
ATOM   1019  N   LYS B  24      18.327  24.340  29.347  1.00 18.87           N
ATOM   1020  CA  LYS B  24      18.756  25.441  30.226  1.00 21.96           C
ATOM   1021  C   LYS B  24      20.207  25.930  30.039  1.00 21.00           C
ATOM   1022  O   LYS B  24      20.567  27.081  30.304  1.00 21.61           O
ATOM   1023  CB  LYS B  24      18.456  25.044  31.703  1.00 23.68           C
ATOM   1024  CG  LYS B  24      16.956  25.097  32.077  1.00 29.69           C
ATOM   1025  CD  LYS B  24      16.544  24.407  33.429  1.00 34.88           C
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Figure 8-28


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ATOM   1026  CE  LYS B  24      15.010  24.526  33.777  1.00 39.45           C
ATOM   1027  NZ  LYS B  24      14.493  23.773  34.927  1.00 41.87           N
ATOM   1028  N   ASP B  25      21.040  25.044  29.503  1.00 19.08           N
ATOM   1029  CA  ASP B  25      22.440  25.350  29.263  1.00 20.79           C
ATOM   1030  C   ASP B  25      22.758  25.601  27.789  1.00 19.77           C
ATOM   1031  O   ASP B  25      23.907  25.469  27.373  1.00 20.06           O
ATOM   1032  CB  ASP B  25      23.305  24.190  29.796  1.00 17.87           C
ATOM   1033  CG  ASP B  25      23.063  22.836  29.175  1.00 20.81           C
ATOM   1034  OD1 ASP B  25      21.975  22.598  28.651  1.00 22.64           O
ATOM   1035  OD2 ASP B  25      23.964  21.991  29.214  1.00 24.79           O
ATOM   1036  N   TYR B  26      21.753  25.866  26.950  1.00 19.06           N
ATOM   1037  CA  TYR B  26      21.990  26.130  25.542  1.00 18.77           C
ATOM   1038  C   TYR B  26      22.027  27.652  25.358  1.00 18.82           C
ATOM   1039  O   TYR B  26      21.066  28.358  25.655  1.00 19.57           O
ATOM   1040  CB  TYR B  26      20.900  25.477  24.712  1.00 16.23           C
ATOM   1041  CG  TYR B  26      21.007  25.766  23.228  1.00 19.16           C
ATOM   1042  CD1 TYR B  26      22.034  25.216  22.492  1.00 20.33           C
ATOM   1043  CD2 TYR B  26      20.097  26.629  22.632  1.00 19.21           C
ATOM   1044  CE1 TYR B  26      22.125  25.531  21.150  1.00 19.71           C
ATOM   1045  CE2 TYR B  26      20.180  26.936  21.294  1.00 18.86           C
ATOM   1046  CZ  TYR B  26      21.184  26.356  20.565  1.00 21.21           C
ATOM   1047  OH  TYR B  26      21.209  26.560  19.204  1.00 23.57           O
HETATM 1048  N   MSE B  27      23.136  28.207  24.891  1.00 18.02           N
HETATM 1049  CA  MSE B  27      23.249  29.645  24.886  1.00 20.01           C
HETATM 1050  C   MSE B  27      22.894  30.253  23.553  1.00 20.43           C
HETATM 1051  O   MSE B  27      23.319  29.791  22.493  1.00 22.74           O
HETATM 1052  CB  MSE B  27      24.648  30.070  25.309  1.00 21.80           C
HETATM 1053  CG  MSE B  27      25.179  29.494  26.646  1.00 24.25           C
HETATM 1054  SE  MSE B  27      24.219  29.995  28.260  1.00 30.76          SE
HETATM 1055  CE  MSE B  27      24.936  31.691  28.317  1.00 17.91           C
ATOM   1056  N   ILE B  28      22.071  31.294  23.642  1.00 21.17           N
ATOM   1057  CA  ILE B  28      21.690  32.092  22.507  1.00 20.03           C
ATOM   1058  C   ILE B  28      22.501  33.383  22.470  1.00 20.64           C
ATOM   1059  O   ILE B  28      22.545  34.162  23.403  1.00 19.83           O
ATOM   1060  CB  ILE B  28      20.168  32.289  22.522  1.00 19.56           C
ATOM   1061  CG1 ILE B  28      19.489  30.935  22.719  1.00 14.81           C
ATOM   1062  CG2 ILE B  28      19.653  32.893  21.195  1.00 17.30           C
ATOM   1063  CD1 ILE B  28      17.993  31.054  22.978  1.00 14.38           C
ATOM   1064  N   THR B  29      23.235  33.585  21.364  1.00 22.56           N
ATOM   1065  CA  THR B  29      24.048  34.777  21.117  1.00 21.92           C
ATOM   1066  C   THR B  29      23.167  35.926  20.723  1.00 21.18           C
ATOM   1067  O   THR B  29      22.235  35.744  19.926  1.00 24.05           O
ATOM   1068  CB  THR B  29      25.003  34.540  19.949  1.00 24.32           C
ATOM   1069  OG1 THR B  29      25.751  33.393  20.310  1.00 26.19           O
ATOM   1070  CG2 THR B  29      25.901  35.743  19.657  1.00 23.45           C
ATOM   1071  N   LEU B  30      23.485  37.110  21.229  1.00 19.18           N
ATOM   1072  CA  LEU B  30      22.694  38.278  20.928  1.00 19.42           C
ATOM   1073  C   LEU B  30      23.612  39.444  21.123  1.00 20.84           C
ATOM   1074  O   LEU B  30      24.251  39.604  22.155  1.00 22.59           O
ATOM   1075  CB  LEU B  30      21.486  38.458  21.822  1.00 16.57           C
ATOM   1076  CG  LEU B  30      20.712  39.739  21.692  1.00 17.65           C
ATOM   1077  CD1 LEU B  30      19.907  39.690  20.405  1.00 15.54           C
ATOM   1078  CD2 LEU B  30      19.875  40.004  22.946  1.00 14.12           C
ATOM   1079  N   LYS B  31      23.641  40.271  20.085  1.00 21.41           N
ATOM   1080  CA  LYS B  31      24.340  41.533  20.142  1.00 22.33           C
ATOM   1081  C   LYS B  31      23.462  42.478  20.918  1.00 21.90           C
ATOM   1082  O   LYS B  31      22.714  43.295  20.370  1.00 24.57           O
ATOM   1083  CB  LYS B  31      24.642  42.093  18.754  1.00 21.18           C
ATOM   1084  CG  LYS B  31      25.844  41.479  18.111  1.00 21.89           C
ATOM   1085  CD  LYS B  31      25.551  41.360  16.647  1.00 29.30           C
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Figure 8-29

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ATOM   1086  CE  LYS B  31      26.741  40.957  15.808  1.00 31.29           C
ATOM   1087  NZ  LYS B  31      27.628  42.105  15.688  1.00 39.41           N
ATOM   1088  N   TYR B  32      23.572  42.299  22.227  1.00 21.32           N
ATOM   1089  CA  TYR B  32      22.800  43.101  23.138  1.00 19.60           C
ATOM   1090  C   TYR B  32      23.198  44.586  22.981  1.00 19.96           C
ATOM   1091  O   TYR B  32      24.384  44.940  22.977  1.00 20.37           O
ATOM   1092  CB  TYR B  32      23.094  42.513  24.532  1.00 17.35           C
ATOM   1093  CG  TYR B  32      22.621  43.373  25.710  1.00 17.26           C
ATOM   1094  CD1 TYR B  32      21.298  43.297  26.107  1.00 15.20           C
ATOM   1095  CD2 TYR B  32      23.490  44.280  26.299  1.00 14.00           C
ATOM   1096  CE1 TYR B  32      20.851  44.149  27.086  1.00 13.12           C
ATOM   1097  CE2 TYR B  32      23.013  45.166  27.227  1.00 14.39           C
ATOM   1098  CZ  TYR B  32      21.702  45.070  27.606  1.00 13.82           C
ATOM   1099  OH  TYR B  32      21.213  45.916  28.560  1.00 18.31           O
ATOM   1100  N   VAL B  33      22.179  45.455  22.873  1.00 19.13           N
ATOM   1101  CA  VAL B  33      22.376  46.889  22.818  1.00 19.34           C
ATOM   1102  C   VAL B  33      22.478  47.489  24.223  1.00 22.86           C
ATOM   1103  O   VAL B  33      21.487  47.535  24.979  1.00 23.26           O
ATOM   1104  CB  VAL B  33      21.220  47.609  22.071  1.00 18.33           C
ATOM   1105  CG1 VAL B  33      21.607  49.014  21.732  1.00 17.72           C
ATOM   1106  CG2 VAL B  33      20.868  46.933  20.772  1.00 18.88           C
ATOM   1107  N   PRO B  34      23.669  48.022  24.556  1.00 23.14           N
ATOM   1108  CA  PRO B  34      23.950  48.685  25.814  1.00 25.98           C
ATOM   1109  C   PRO B  34      22.991  49.844  26.052  1.00 27.87           C
ATOM   1110  O   PRO B  34      22.782  50.697  25.173  1.00 28.20           O
ATOM   1111  CB  PRO B  34      25.355  49.247  25.629  1.00 24.52           C
ATOM   1112  CG  PRO B  34      25.947  48.454  24.514  1.00 23.81           C
ATOM   1113  CD  PRO B  34      24.761  48.256  23.617  1.00 23.96           C
ATOM   1114  N   GLY B  35      22.428  49.854  27.265  1.00 27.60           N
ATOM   1115  CA  GLY B  35      21.544  50.919  27.694  1.00 26.85           C
ATOM   1116  C   GLY B  35      20.103  50.509  27.809  1.00 26.95           C
ATOM   1117  O   GLY B  35      19.314  51.234  28.392  1.00 27.06           O
HETATM 1118  N   MSE B  36      19.736  49.361  27.277  1.00 27.66           N
HETATM 1119  CA  MSE B  36      18.444  48.762  27.502  1.00 31.16           C
HETATM 1120  C   MSE B  36      17.873  48.948  28.920  1.00 33.96           C
HETATM 1121  O   MSE B  36      16.708  49.315  29.138  1.00 34.27           O
HETATM 1122  CB  MSE B  36      18.679  47.299  27.225  1.00 34.63           C
HETATM 1123  CG  MSE B  36      17.921  46.622  26.126  1.00 37.69           C
HETATM 1124  SE  MSE B  36      16.954  45.030  26.682  1.00 48.87          SE
HETATM 1125  CE  MSE B  36      16.692  45.161  28.580  1.00 40.22           C
ATOM   1126  N   ASP B  37      18.753  48.712  29.902  1.00 35.95           N
ATOM   1127  CA  ASP B  37      18.421  48.828  31.303  1.00 37.28           C
ATOM   1128  C   ASP B  37      18.228  50.272  31.758  1.00 38.57           C
ATOM   1129  O   ASP B  37      17.189  50.545  32.368  1.00 42.23           O
ATOM   1130  CB  ASP B  37      19.407  48.058  32.203  1.00 38.21           C
ATOM   1131  CG  ASP B  37      20.907  48.280  32.005  1.00 42.18           C
ATOM   1132  OD1 ASP B  37      21.288  49.092  31.150  1.00 44.69           O
ATOM   1133  OD2 ASP B  37      21.709  47.641  32.708  1.00 43.60           O
ATOM   1134  N   VAL B  38      19.111  51.237  31.458  1.00 36.46           N
ATOM   1135  CA  VAL B  38      18.974  52.585  32.008  1.00 34.42           C
ATOM   1136  C   VAL B  38      18.360  53.701  31.150  1.00 35.48           C
ATOM   1137  O   VAL B  38      17.844  54.706  31.662  1.00 35.46           O
ATOM   1138  CB  VAL B  38      20.314  53.047  32.623  1.00 33.96           C
ATOM   1139  CG1 VAL B  38      20.656  52.110  33.757  1.00 33.39           C
ATOM   1140  CG2 VAL B  38      21.452  53.127  31.638  1.00 30.40           C
ATOM   1141  N   LEU B  39      18.466  53.536  29.826  1.00 34.58           N
ATOM   1142  CA  LEU B  39      18.173  54.590  28.859  1.00 33.84           C
ATOM   1143  C   LEU B  39      16.770  54.521  28.304  1.00 34.39           C
ATOM   1144  O   LEU B  39      16.234  53.407  28.274  1.00 37.21           O
ATOM   1145  CB  LEU B  39      19.106  54.513  27.672  1.00 31.59           C
```

Figure 8-30

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ATOM   1146  CG  LEU B  39      20.516  54.934  27.836  1.00 30.49           C
ATOM   1147  CD1 LEU B  39      21.233  54.571  26.544  1.00 30.11           C
ATOM   1148  CD2 LEU B  39      20.556  56.416  28.187  1.00 28.81           C
ATOM   1149  N   PRO B  40      16.124  55.613  27.821  1.00 33.22           N
ATOM   1150  CA  PRO B  40      14.743  55.564  27.336  1.00 32.18           C
ATOM   1151  C   PRO B  40      14.595  54.656  26.104  1.00 31.61           C
ATOM   1152  O   PRO B  40      15.515  54.575  25.295  1.00 32.07           O
ATOM   1153  CB  PRO B  40      14.498  57.028  27.054  1.00 31.41           C
ATOM   1154  CG  PRO B  40      15.395  57.749  28.027  1.00 32.72           C
ATOM   1155  CD  PRO B  40      16.655  56.977  27.813  1.00 33.34           C
ATOM   1156  N   SER B  41      13.487  53.949  25.885  1.00 31.04           N
ATOM   1157  CA  SER B  41      13.422  52.973  24.819  1.00 32.48           C
ATOM   1158  C   SER B  41      13.785  53.436  23.428  1.00 32.31           C
ATOM   1159  O   SER B  41      14.301  52.651  22.638  1.00 30.86           O
ATOM   1160  CB  SER B  41      12.119  52.197  24.820  1.00 34.06           C
ATOM   1161  OG  SER B  41      10.984  53.037  24.872  1.00 39.11           O
ATOM   1162  N   HIS B  42      13.622  54.747  23.191  1.00 34.63           N
ATOM   1163  CA  HIS B  42      13.911  55.363  21.888  1.00 36.02           C
ATOM   1164  C   HIS B  42      15.396  55.300  21.511  1.00 36.52           C
ATOM   1165  O   HIS B  42      15.780  55.228  20.327  1.00 34.40           O
ATOM   1166  CB  HIS B  42      13.316  56.805  21.755  1.00 34.27           C
ATOM   1167  CG  HIS B  42      13.946  57.935  22.576  1.00 34.59           C
ATOM   1168  ND1 HIS B  42      13.588  58.408  23.772  1.00 36.14           N
ATOM   1169  CD2 HIS B  42      15.013  58.687  22.154  1.00 32.00           C
ATOM   1170  CE1 HIS B  42      14.381  59.396  24.117  1.00 32.43           C
ATOM   1171  NE2 HIS B  42      15.227  59.539  23.124  1.00 35.02           N
ATOM   1172  N   CYS B  43      16.177  55.249  22.615  1.00 35.96           N
ATOM   1173  CA  CYS B  43      17.627  55.122  22.565  1.00 35.90           C
ATOM   1174  C   CYS B  43      18.176  53.799  22.054  1.00 32.86           C
ATOM   1175  O   CYS B  43      19.347  53.782  21.649  1.00 33.40           O
ATOM   1176  CB  CYS B  43      18.339  55.448  23.910  1.00 40.38           C
ATOM   1177  SG  CYS B  43      18.099  57.127  24.542  1.00 45.68           S
ATOM   1178  N   TRP B  44      17.380  52.707  22.075  1.00 29.25           N
ATOM   1179  CA  TRP B  44      17.913  51.374  21.831  1.00 25.51           C
ATOM   1180  C   TRP B  44      17.009  50.463  21.066  1.00 24.22           C
ATOM   1181  O   TRP B  44      17.544  49.594  20.406  1.00 26.02           O
ATOM   1182  CB  TRP B  44      18.375  50.661  23.113  1.00 21.99           C
ATOM   1183  CG  TRP B  44      17.351  50.644  24.234  1.00 20.34           C
ATOM   1184  CD1 TRP B  44      17.361  51.632  25.183  1.00 18.11           C
ATOM   1185  CD2 TRP B  44      16.297  49.745  24.363  1.00 19.23           C
ATOM   1186  NE1 TRP B  44      16.293  51.390  25.908  1.00 19.12           N
ATOM   1187  CE2 TRP B  44      15.635  50.281  25.471  1.00 18.20           C
ATOM   1188  CE3 TRP B  44      15.892  48.551  23.795  1.00 15.22           C
ATOM   1189  CZ2 TRP B  44      14.532  49.622  26.000  1.00 14.99           C
ATOM   1190  CZ3 TRP B  44      14.805  47.897  24.324  1.00 13.45           C
ATOM   1191  CH2 TRP B  44      14.130  48.434  25.405  1.00 15.50           C
ATOM   1192  N   ILE B  45      15.680  50.626  21.096  1.00 24.85           N
ATOM   1193  CA  ILE B  45      14.726  49.656  20.539  1.00 25.50           C
ATOM   1194  C   ILE B  45      14.926  49.254  19.094  1.00 26.34           C
ATOM   1195  O   ILE B  45      14.724  48.086  18.762  1.00 28.11           O
ATOM   1196  CB  ILE B  45      13.231  50.055  20.773  1.00 26.28           C
ATOM   1197  CG1 ILE B  45      12.358  48.838  20.592  1.00 24.31           C
ATOM   1198  CG2 ILE B  45      12.716  51.206  19.885  1.00 25.51           C
ATOM   1199  CD1 ILE B  45      12.688  47.633  21.486  1.00 19.41           C
ATOM   1200  N   SER B  46      15.336  50.233  18.274  1.00 28.06           N
ATOM   1201  CA  SER B  46      15.623  50.071  16.851  1.00 28.67           C
ATOM   1202  C   SER B  46      16.739  49.059  16.553  1.00 27.51           C
ATOM   1203  O   SER B  46      16.558  48.113  15.773  1.00 26.90           O
ATOM   1204  CB  SER B  46      15.933  51.472  16.250  1.00 28.71           C
ATOM   1205  OG  SER B  46      16.259  51.414  14.871  1.00 31.35           O
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Figure 8-31

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ATOM   1206  N   GLU B  47      17.902  49.210  17.203  1.00 26.77           N
ATOM   1207  CA  GLU B  47      18.910  48.173  17.142  1.00 27.22           C
ATOM   1208  C   GLU B  47      18.555  46.912  17.906  1.00 23.80           C
ATOM   1209  O   GLU B  47      19.011  45.850  17.513  1.00 24.85           O
ATOM   1210  CB  GLU B  47      20.209  48.703  17.683  1.00 30.36           C
ATOM   1211  CG  GLU B  47      21.460  47.909  17.269  1.00 31.64           C
ATOM   1212  CD  GLU B  47      21.718  47.840  15.774  1.00 31.93           C
ATOM   1213  OE1 GLU B  47      21.267  48.726  15.034  1.00 32.82           O
ATOM   1214  OE2 GLU B  47      22.391  46.892  15.366  1.00 31.60           O
HETATM 1215  N   MSE B  48      17.739  46.958  18.958  1.00 23.65           N
HETATM 1216  CA  MSE B  48      17.401  45.755  19.709  1.00 21.94           C
HETATM 1217  C   MSE B  48      16.511  44.916  18.837  1.00 22.24           C
HETATM 1218  O   MSE B  48      16.819  43.732  18.731  1.00 24.91           O
HETATM 1219  CB  MSE B  48      16.783  46.061  21.080  1.00 22.86           C
HETATM 1220  CG  MSE B  48      16.875  44.981  22.173  1.00 24.51           C
HETATM 1221  SE  MSE B  48      18.597  44.203  22.615  1.00 30.61          SE
HETATM 1222  CE  MSE B  48      17.982  42.661  21.922  1.00 26.74           C
ATOM   1223  N   VAL B  49      15.506  45.445  18.110  1.00 21.88           N
ATOM   1224  CA  VAL B  49      14.661  44.597  17.276  1.00 20.25           C
ATOM   1225  C   VAL B  49      15.387  43.973  16.098  1.00 20.18           C
ATOM   1226  O   VAL B  49      15.120  42.815  15.780  1.00 22.62           O
ATOM   1227  CB  VAL B  49      13.351  45.252  16.813  1.00 23.22           C
ATOM   1228  CG1 VAL B  49      12.455  45.562  17.992  1.00 24.62           C
ATOM   1229  CG2 VAL B  49      13.551  46.527  16.025  1.00 23.30           C
ATOM   1230  N   VAL B  50      16.363  44.655  15.484  1.00 19.52           N
ATOM   1231  CA  VAL B  50      17.179  44.087  14.408  1.00 19.02           C
ATOM   1232  C   VAL B  50      18.005  42.916  14.897  1.00 19.73           C
ATOM   1233  O   VAL B  50      18.091  41.872  14.232  1.00 19.76           O
ATOM   1234  CB  VAL B  50      18.110  45.171  13.808  1.00 18.29           C
ATOM   1235  CG1 VAL B  50      19.181  44.607  12.925  1.00 16.52           C
ATOM   1236  CG2 VAL B  50      17.290  46.136  13.024  1.00 18.74           C
ATOM   1237  N   GLN B  51      18.617  43.151  16.064  1.00 17.95           N
ATOM   1238  CA  GLN B  51      19.447  42.130  16.677  1.00 18.39           C
ATOM   1239  C   GLN B  51      18.645  40.938  17.084  1.00 16.66           C
ATOM   1240  O   GLN B  51      19.056  39.827  16.830  1.00 18.39           O
ATOM   1241  CB  GLN B  51      20.264  42.655  17.851  1.00 18.87           C
ATOM   1242  CG  GLN B  51      21.265  43.713  17.440  1.00 18.55           C
ATOM   1243  CD  GLN B  51      22.253  43.283  16.370  1.00 23.83           C
ATOM   1244  OE1 GLN B  51      22.400  42.141  15.918  1.00 23.92           O
ATOM   1245  NE2 GLN B  51      23.019  44.265  15.958  1.00 27.04           N
ATOM   1246  N   LEU B  52      17.481  41.149  17.652  1.00 16.16           N
ATOM   1247  CA  LEU B  52      16.615  40.053  18.010  1.00 17.66           C
ATOM   1248  C   LEU B  52      16.106  39.302  16.810  1.00 18.23           C
ATOM   1249  O   LEU B  52      16.012  38.080  16.844  1.00 18.09           O
ATOM   1250  CB  LEU B  52      15.412  40.576  18.771  1.00 19.12           C
ATOM   1251  CG  LEU B  52      15.665  40.840  20.232  1.00 20.87           C
ATOM   1252  CD1 LEU B  52      14.609  41.767  20.734  1.00 20.47           C
ATOM   1253  CD2 LEU B  52      15.692  39.553  21.037  1.00 21.69           C
ATOM   1254  N   SER B  53      15.797  40.014  15.717  1.00 20.42           N
ATOM   1255  CA  SER B  53      15.410  39.376  14.469  1.00 18.47           C
ATOM   1256  C   SER B  53      16.491  38.428  13.973  1.00 18.27           C
ATOM   1257  O   SER B  53      16.259  37.257  13.692  1.00 17.53           O
ATOM   1258  CB  SER B  53      15.188  40.496  13.523  1.00 21.19           C
ATOM   1259  OG  SER B  53      14.858  39.866  12.317  1.00 22.45           O
ATOM   1260  N   ASP B  54      17.729  38.892  13.962  1.00 21.01           N
ATOM   1261  CA  ASP B  54      18.811  38.060  13.483  1.00 25.15           C
ATOM   1262  C   ASP B  54      19.040  36.841  14.339  1.00 24.43           C
ATOM   1263  O   ASP B  54      19.279  35.764  13.782  1.00 24.72           O
ATOM   1264  CB  ASP B  54      20.170  38.731  13.462  1.00 32.20           C
ATOM   1265  CG  ASP B  54      20.366  40.017  12.671  1.00 44.10           C
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Figure 8-32

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ATOM   1266  OD1 ASP B  54      19.508  40.411  11.838  1.00 48.06           O
ATOM   1267  OD2 ASP B  54      21.429  40.630  12.924  1.00 50.40           O
ATOM   1268  N   SER B  55      19.025  37.009  15.674  1.00 21.94           N
ATOM   1269  CA  SER B  55      19.197  35.872  16.589  1.00 21.29           C
ATOM   1270  C   SER B  55      18.036  34.884  16.516  1.00 19.86           C
ATOM   1271  O   SER B  55      18.259  33.675  16.567  1.00 20.94           O
ATOM   1272  CB  SER B  55      19.356  36.295  18.052  1.00 18.68           C
ATOM   1273  OG  SER B  55      20.384  37.208  18.406  1.00 18.26           O
ATOM   1274  N   LEU B  56      16.789  35.362  16.374  1.00 20.32           N
ATOM   1275  CA  LEU B  56      15.647  34.453  16.343  1.00 20.44           C
ATOM   1276  C   LEU B  56      15.628  33.735  15.025  1.00 21.16           C
ATOM   1277  O   LEU B  56      15.299  32.552  14.968  1.00 20.64           O
ATOM   1278  CB  LEU B  56      14.335  35.169  16.568  1.00 19.08           C
ATOM   1279  CG  LEU B  56      13.967  35.545  17.993  1.00 19.76           C
ATOM   1280  CD1 LEU B  56      12.809  36.497  18.033  1.00 18.12           C
ATOM   1281  CD2 LEU B  56      13.621  34.308  18.773  1.00 17.63           C
ATOM   1282  N   THR B  57      16.081  34.451  13.984  1.00 22.55           N
ATOM   1283  CA  THR B  57      16.144  33.901  12.624  1.00 23.77           C
ATOM   1284  C   THR B  57      17.169  32.775  12.599  1.00 25.31           C
ATOM   1285  O   THR B  57      16.904  31.674  12.109  1.00 28.36           O
ATOM   1286  CB  THR B  57      16.420  35.019  11.581  1.00 22.83           C
ATOM   1287  OG1 THR B  57      15.245  35.800  11.520  1.00 20.28           O
ATOM   1288  CG2 THR B  57      16.608  34.496  10.209  1.00 22.98           C
ATOM   1289  N   ASP B  58      18.331  32.975  13.229  1.00 27.29           N
ATOM   1290  CA  ASP B  58      19.328  31.934  13.394  1.00 25.16           C
ATOM   1291  C   ASP B  58      18.874  30.781  14.238  1.00 22.74           C
ATOM   1292  O   ASP B  58      19.128  29.640  13.909  1.00 20.50           O
ATOM   1293  CB  ASP B  58      20.510  32.549  14.059  1.00 32.90           C
ATOM   1294  CG  ASP B  58      21.367  33.343  13.098  1.00 40.22           C
ATOM   1295  OD1 ASP B  58      21.635  32.807  11.999  1.00 47.28           O
ATOM   1296  OD2 ASP B  58      21.780  34.468  13.458  1.00 42.79           O
ATOM   1297  N   LEU B  59      18.174  31.090  15.328  1.00 22.88           N
ATOM   1298  CA  LEU B  59      17.597  30.066  16.166  1.00 22.01           C
ATOM   1299  C   LEU B  59      16.596  29.206  15.391  1.00 22.75           C
ATOM   1300  O   LEU B  59      16.642  27.981  15.498  1.00 24.25           O
ATOM   1301  CB  LEU B  59      16.984  30.711  17.389  1.00 21.26           C
ATOM   1302  CG  LEU B  59      16.544  29.703  18.408  1.00 21.05           C
ATOM   1303  CD1 LEU B  59      17.733  28.955  19.020  1.00 20.13           C
ATOM   1304  CD2 LEU B  59      15.718  30.419  19.413  1.00 20.68           C
ATOM   1305  N   LEU B  60      15.729  29.754  14.537  1.00 22.30           N
ATOM   1306  CA  LEU B  60      14.838  28.912  13.776  1.00 21.18           C
ATOM   1307  C   LEU B  60      15.559  27.884  12.897  1.00 24.69           C
ATOM   1308  O   LEU B  60      15.084  26.761  12.702  1.00 27.59           O
ATOM   1309  CB  LEU B  60      13.949  29.829  12.982  1.00 20.34           C
ATOM   1310  CG  LEU B  60      12.805  29.256  12.208  1.00 15.11           C
ATOM   1311  CD1 LEU B  60      11.775  28.689  13.124  1.00 14.00           C
ATOM   1312  CD2 LEU B  60      12.216  30.351  11.405  1.00 15.62           C
ATOM   1313  N   ASP B  61      16.768  28.142  12.405  1.00 28.19           N
ATOM   1314  CA  ASP B  61      17.425  27.134  11.587  1.00 31.01           C
ATOM   1315  C   ASP B  61      17.898  25.925  12.380  1.00 30.42           C
ATOM   1316  O   ASP B  61      18.293  24.903  11.836  1.00 30.78           O
ATOM   1317  CB  ASP B  61      18.486  27.766  10.638  1.00 40.38           C
ATOM   1318  CG  ASP B  61      20.011  27.910  10.913  1.00 49.60           C
ATOM   1319  OD1 ASP B  61      20.632  27.086  11.630  1.00 52.10           O
ATOM   1320  OD2 ASP B  61      20.602  28.852  10.340  1.00 54.11           O
ATOM   1321  N   LYS B  62      17.841  26.023  13.706  1.00 29.72           N
ATOM   1322  CA  LYS B  62      18.282  24.972  14.586  1.00 26.53           C
ATOM   1323  C   LYS B  62      17.227  23.920  14.754  1.00 26.40           C
ATOM   1324  O   LYS B  62      17.553  22.835  15.224  1.00 28.09           O
ATOM   1325  CB  LYS B  62      18.655  25.534  15.953  1.00 25.89           C
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Figure 8-33

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ATOM   1326  CG  LYS B  62      19.865  26.451  15.996  1.00 24.99           C
ATOM   1327  CD  LYS B  62      21.053  25.810  15.308  1.00 26.66           C
ATOM   1328  CE  LYS B  62      22.198  26.806  15.251  1.00 28.58           C
ATOM   1329  NZ  LYS B  62      21.868  27.957  14.431  1.00 34.52           N
ATOM   1330  N   PHE B  63      15.986  24.225  14.389  1.00 26.48           N
ATOM   1331  CA  PHE B  63      14.862  23.316  14.568  1.00 29.27           C
ATOM   1332  C   PHE B  63      14.293  22.916  13.220  1.00 31.78           C
ATOM   1333  O   PHE B  63      14.573  23.581  12.227  1.00 34.39           O
ATOM   1334  CB  PHE B  63      13.744  23.920  15.427  1.00 24.13           C
ATOM   1335  CG  PHE B  63      14.261  24.236  16.809  1.00 23.83           C
ATOM   1336  CD1 PHE B  63      14.269  23.261  17.761  1.00 20.94           C
ATOM   1337  CD2 PHE B  63      14.811  25.488  17.066  1.00 25.00           C
ATOM   1338  CE1 PHE B  63      14.872  23.535  18.964  1.00 23.54           C
ATOM   1339  CE2 PHE B  63      15.444  25.741  18.263  1.00 22.33           C
ATOM   1340  CZ  PHE B  63      15.467  24.752  19.211  1.00 21.46           C
ATOM   1341  N   SER B  64      13.565  21.791  13.203  1.00 35.96           N
ATOM   1342  CA  SER B  64      12.847  21.251  12.047  1.00 41.24           C
ATOM   1343  C   SER B  64      11.362  21.237  12.401  1.00 44.87           C
ATOM   1344  O   SER B  64      11.045  21.210  13.593  1.00 45.47           O
ATOM   1345  CB  SER B  64      13.299  19.810  11.723  1.00 39.81           C
ATOM   1346  OG  SER B  64      14.690  19.659  11.441  1.00 41.15           O
ATOM   1347  N   ASN B  65      10.393  21.257  11.464  1.00 50.28           N
ATOM   1348  CA  ASN B  65       8.980  21.293  11.878  1.00 53.31           C
ATOM   1349  C   ASN B  65       8.304  19.970  12.291  1.00 53.88           C
ATOM   1350  O   ASN B  65       8.619  18.877  11.815  1.00 53.27           O
ATOM   1351  CB  ASN B  65       8.137  22.121  10.899  1.00 55.21           C
ATOM   1352  CG  ASN B  65       6.847  22.674  11.525  1.00 58.28           C
ATOM   1353  OD1 ASN B  65       5.829  22.845  10.846  1.00 62.80           O
ATOM   1354  ND2 ASN B  65       6.802  22.997  12.821  1.00 58.83           N
ATOM   1355  N   ILE B  66       7.402  20.111  13.274  1.00 55.78           N
ATOM   1356  CA  ILE B  66       6.604  19.028  13.857  1.00 58.20           C
ATOM   1357  C   ILE B  66       5.128  19.413  13.732  1.00 59.99           C
ATOM   1358  O   ILE B  66       4.679  20.439  14.266  1.00 59.98           O
ATOM   1359  CB  ILE B  66       6.916  18.864  15.373  1.00 58.00           C
ATOM   1360  CG1 ILE B  66       8.393  18.635  15.673  1.00 56.77           C
ATOM   1361  CG2 ILE B  66       6.119  17.713  15.950  1.00 58.43           C
ATOM   1362  CD1 ILE B  66       8.729  18.733  17.169  1.00 53.61           C
ATOM   1363  N   SER B  67       4.387  18.545  13.027  1.00 62.59           N
ATOM   1364  CA  SER B  67       2.945  18.687  12.803  1.00 65.18           C
ATOM   1365  C   SER B  67       2.049  18.114  13.935  1.00 66.39           C
ATOM   1366  O   SER B  67       1.110  17.339  13.725  1.00 68.18           O
ATOM   1367  CB  SER B  67       2.632  18.133  11.385  1.00 65.71           C
ATOM   1368  OG  SER B  67       3.288  16.912  10.995  1.00 67.79           O
ATOM   1369  N   GLU B  68       2.307  18.549  15.184  1.00 66.59           N
ATOM   1370  CA  GLU B  68       1.793  17.929  16.415  1.00 65.52           C
ATOM   1371  C   GLU B  68       0.895  18.865  17.238  1.00 66.78           C
ATOM   1372  O   GLU B  68      -0.333  18.715  17.307  1.00 67.15           O
ATOM   1373  CB  GLU B  68       2.977  17.471  17.301  1.00 66.40           C
ATOM   1374  CG  GLU B  68       2.568  17.163  18.743  1.00 67.84           C
ATOM   1375  CD  GLU B  68       3.745  16.736  19.622  1.00 69.12           C
ATOM   1376  OE1 GLU B  68       4.931  16.661  19.119  1.00 70.46           O
ATOM   1377  OE2 GLU B  68       3.552  16.451  20.865  1.00 71.34           O
ATOM   1378  N   GLY B  69       1.582  19.807  17.897  1.00 65.16           N
ATOM   1379  CA  GLY B  69       1.015  20.935  18.626  1.00 63.26           C
ATOM   1380  C   GLY B  69       2.019  22.049  18.382  1.00 60.63           C
ATOM   1381  O   GLY B  69       2.666  22.081  17.308  1.00 60.82           O
ATOM   1382  N   LEU B  70       2.179  22.963  19.355  1.00 57.50           N
ATOM   1383  CA  LEU B  70       3.254  23.950  19.225  1.00 53.07           C
ATOM   1384  C   LEU B  70       4.610  23.233  19.244  1.00 50.38           C
ATOM   1385  O   LEU B  70       4.879  22.324  20.040  1.00 53.95           O
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Figure 8-34

ATOM	1386	CB	LEU	B	70	3.243	25.033	20.295	1.00	52.74	C
ATOM	1387	CG	LEU	B	70	2.243	26.184	20.332	1.00	54.01	C
ATOM	1388	CD1	LEU	B	70	2.326	26.991	19.014	1.00	54.05	C
ATOM	1389	CD2	LEU	B	70	0.834	25.683	20.698	1.00	55.75	C
ATOM	1390	N	SER	B	71	5.437	23.543	18.271	1.00	43.22	N
ATOM	1391	CA	SER	B	71	6.788	23.107	18.347	1.00	37.10	C
ATOM	1392	C	SER	B	71	7.676	24.348	18.452	1.00	35.41	C
ATOM	1393	O	SER	B	71	7.223	25.469	18.195	1.00	34.32	O
ATOM	1394	CB	SER	B	71	7.030	22.242	17.147	1.00	36.36	C
ATOM	1395	OG	SER	B	71	6.753	22.899	15.934	1.00	36.82	O
ATOM	1396	N	ASN	B	72	8.946	24.206	18.876	1.00	33.26	N
ATOM	1397	CA	ASN	B	72	9.888	25.327	18.974	1.00	28.70	C
ATOM	1398	C	ASN	B	72	10.013	26.017	17.631	1.00	25.92	C
ATOM	1399	O	ASN	B	72	10.086	27.234	17.591	1.00	25.46	O
ATOM	1400	CB	ASN	B	72	11.281	24.862	19.462	1.00	28.21	C
ATOM	1401	CG	ASN	B	72	11.365	24.292	20.880	1.00	26.47	C
ATOM	1402	OD1	ASN	B	72	10.592	24.638	21.764	1.00	25.38	O
ATOM	1403	ND2	ASN	B	72	12.284	23.373	21.160	1.00	26.66	N
ATOM	1404	N	TYR	B	73	9.968	25.221	16.547	1.00	26.29	N
ATOM	1405	CA	TYR	B	73	9.940	25.723	15.179	1.00	26.54	C
ATOM	1406	C	TYR	B	73	8.760	26.639	14.993	1.00	23.80	C
ATOM	1407	O	TYR	B	73	8.967	27.809	14.726	1.00	27.19	O
ATOM	1408	CB	TYR	B	73	9.881	24.631	14.075	1.00	28.15	C
ATOM	1409	CG	TYR	B	73	10.162	25.129	12.647	1.00	28.60	C
ATOM	1410	CD1	TYR	B	73	9.210	25.828	11.901	1.00	29.58	C
ATOM	1411	CD2	TYR	B	73	11.426	24.929	12.122	1.00	30.26	C
ATOM	1412	CE1	TYR	B	73	9.566	26.391	10.690	1.00	29.50	C
ATOM	1413	CE2	TYR	B	73	11.783	25.467	10.898	1.00	31.02	C
ATOM	1414	CZ	TYR	B	73	10.855	26.215	10.209	1.00	32.38	C
ATOM	1415	OH	TYR	B	73	11.245	26.802	9.014	1.00	36.91	O
ATOM	1416	N	SER	B	74	7.535	26.185	15.145	1.00	23.20	N
ATOM	1417	CA	SER	B	74	6.402	27.077	15.028	1.00	24.27	C
ATOM	1418	C	SER	B	74	6.449	28.270	15.935	1.00	23.26	C
ATOM	1419	O	SER	B	74	6.039	29.360	15.572	1.00	25.85	O
ATOM	1420	CB	SER	B	74	5.156	26.342	15.357	1.00	25.27	C
ATOM	1421	OG	SER	B	74	5.173	25.254	14.460	1.00	32.42	O
ATOM	1422	N	ILE	B	75	6.958	28.120	17.146	1.00	25.08	N
ATOM	1423	CA	ILE	B	75	6.913	29.248	18.057	1.00	23.59	C
ATOM	1424	C	ILE	B	75	7.908	30.294	17.620	1.00	21.89	C
ATOM	1425	O	ILE	B	75	7.509	31.437	17.519	1.00	21.19	O
ATOM	1426	CB	ILE	B	75	7.150	28.785	19.482	1.00	23.07	C
ATOM	1427	CG1	ILE	B	75	5.984	27.956	19.962	1.00	23.49	C
ATOM	1428	CG2	ILE	B	75	7.272	29.985	20.397	1.00	22.81	C
ATOM	1429	CD1	ILE	B	75	6.254	27.309	21.343	1.00	21.59	C
ATOM	1430	N	ILE	B	76	9.149	29.881	17.347	1.00	21.79	N
ATOM	1431	CA	ILE	B	76	10.226	30.789	16.994	1.00	22.16	C
ATOM	1432	C	ILE	B	76	9.830	31.465	15.705	1.00	23.36	C
ATOM	1433	O	ILE	B	76	9.898	32.679	15.673	1.00	26.09	O
ATOM	1434	CB	ILE	B	76	11.611	30.123	16.831	1.00	21.17	C
ATOM	1435	CG1	ILE	B	76	12.075	29.444	18.092	1.00	19.74	C
ATOM	1436	CG2	ILE	B	76	12.661	31.169	16.489	1.00	18.62	C
ATOM	1437	CD1	ILE	B	76	13.143	28.388	17.846	1.00	17.66	C
ATOM	1438	N	ASP	B	77	9.353	30.734	14.702	1.00	23.97	N
ATOM	1439	CA	ASP	B	77	8.866	31.293	13.456	1.00	25.97	C
ATOM	1440	C	ASP	B	77	7.856	32.411	13.657	1.00	26.70	C
ATOM	1441	O	ASP	B	77	8.065	33.525	13.187	1.00	28.84	O
ATOM	1442	CB	ASP	B	77	8.223	30.179	12.680	1.00	28.57	C
ATOM	1443	CG	ASP	B	77	8.018	30.507	11.212	1.00	32.25	C
ATOM	1444	OD1	ASP	B	77	8.957	31.036	10.598	1.00	34.07	O
ATOM	1445	OD2	ASP	B	77	6.927	30.224	10.704	1.00	32.50	O

Figure 8-35

ATOM	1446	N	LYS	B	78	6.797	32.211	14.443	1.00	28.77	N
ATOM	1447	CA	LYS	B	78	5.891	33.285	14.868	1.00	28.31	C
ATOM	1448	C	LYS	B	78	6.596	34.463	15.571	1.00	26.90	C
ATOM	1449	O	LYS	B	78	6.221	35.629	15.449	1.00	26.22	O
ATOM	1450	CB	LYS	B	78	4.861	32.589	15.762	1.00	32.30	C
ATOM	1451	CG	LYS	B	78	3.767	33.491	16.290	1.00	41.29	C
ATOM	1452	CD	LYS	B	78	2.746	32.676	17.100	1.00	49.72	C
ATOM	1453	CE	LYS	B	78	1.564	33.546	17.666	1.00	53.37	C
ATOM	1454	NZ	LYS	B	78	0.551	32.773	18.406	1.00	54.23	N
ATOM	1455	N	LEU	B	79	7.663	34.218	16.330	1.00	25.35	N
ATOM	1456	CA	LEU	B	79	8.352	35.299	17.007	1.00	23.52	C
ATOM	1457	C	LEU	B	79	9.151	36.141	16.063	1.00	22.42	C
ATOM	1458	O	LEU	B	79	9.249	37.348	16.219	1.00	20.72	O
ATOM	1459	CB	LEU	B	79	9.292	34.752	18.074	1.00	23.66	C
ATOM	1460	CG	LEU	B	79	8.739	33.917	19.241	1.00	21.39	C
ATOM	1461	CD1	LEU	B	79	9.823	33.698	20.260	1.00	17.54	C
ATOM	1462	CD2	LEU	B	79	7.579	34.608	19.911	1.00	21.67	C
ATOM	1463	N	VAL	B	80	9.727	35.426	15.094	1.00	25.43	N
ATOM	1464	CA	VAL	B	80	10.474	35.983	13.952	1.00	25.77	C
ATOM	1465	C	VAL	B	80	9.566	36.918	13.200	1.00	25.42	C
ATOM	1466	O	VAL	B	80	9.948	38.052	12.971	1.00	26.43	O
ATOM	1467	CB	VAL	B	80	10.989	34.920	12.949	1.00	24.61	C
ATOM	1468	CG1	VAL	B	80	11.693	35.588	11.801	1.00	26.74	C
ATOM	1469	CG2	VAL	B	80	12.018	33.999	13.521	1.00	24.19	C
ATOM	1470	N	ASN	B	81	8.352	36.466	12.893	1.00	27.82	N
ATOM	1471	CA	ASN	B	81	7.420	37.299	12.163	1.00	29.77	C
ATOM	1472	C	ASN	B	81	6.999	38.527	12.964	1.00	29.38	C
ATOM	1473	O	ASN	B	81	6.937	39.593	12.377	1.00	32.14	O
ATOM	1474	CB	ASN	B	81	6.221	36.505	11.562	1.00	31.24	C
ATOM	1475	CG	ASN	B	81	6.543	35.379	10.564	1.00	33.72	C
ATOM	1476	OD1	ASN	B	81	7.608	35.271	9.962	1.00	34.16	O
ATOM	1477	ND2	ASN	B	81	5.614	34.454	10.332	1.00	37.55	N
ATOM	1478	N	ILE	B	82	6.761	38.515	14.283	1.00	30.06	N
ATOM	1479	CA	ILE	B	82	6.418	39.713	15.057	1.00	27.77	C
ATOM	1480	C	ILE	B	82	7.591	40.672	15.019	1.00	28.50	C
ATOM	1481	O	ILE	B	82	7.388	41.866	14.826	1.00	30.63	O
ATOM	1482	CB	ILE	B	82	6.164	39.318	16.534	1.00	27.91	C
ATOM	1483	CG1	ILE	B	82	4.880	38.557	16.625	1.00	29.24	C
ATOM	1484	CG2	ILE	B	82	6.192	40.458	17.555	1.00	23.22	C
ATOM	1485	CD1	ILE	B	82	4.796	37.771	17.958	1.00	33.77	C
ATOM	1486	N	VAL	B	83	8.833	40.218	15.222	1.00	28.54	N
ATOM	1487	CA	VAL	B	83	9.884	41.192	15.413	1.00	28.60	C
ATOM	1488	C	VAL	B	83	10.348	41.752	14.061	1.00	32.57	C
ATOM	1489	O	VAL	B	83	10.849	42.878	13.989	1.00	32.81	O
ATOM	1490	CB	VAL	B	83	10.975	40.632	16.338	1.00	26.41	C
ATOM	1491	CG1	VAL	B	83	11.972	39.760	15.644	1.00	26.53	C
ATOM	1492	CG2	VAL	B	83	11.609	41.742	17.144	1.00	25.82	C
ATOM	1493	N	ASP	B	84	10.153	40.975	12.980	1.00	33.06	N
ATOM	1494	CA	ASP	B	84	10.383	41.446	11.632	1.00	34.79	C
ATOM	1495	C	ASP	B	84	9.332	42.450	11.205	1.00	34.82	C
ATOM	1496	O	ASP	B	84	9.665	43.271	10.357	1.00	36.49	O
ATOM	1497	CB	ASP	B	84	10.391	40.329	10.601	1.00	37.40	C
ATOM	1498	CG	ASP	B	84	11.732	39.649	10.403	1.00	41.65	C
ATOM	1499	OD1	ASP	B	84	12.767	40.242	10.726	1.00	45.61	O
ATOM	1500	OD2	ASP	B	84	11.746	38.524	9.895	1.00	45.89	O
ATOM	1501	N	ASP	B	85	8.101	42.430	11.753	1.00	33.73	N
ATOM	1502	CA	ASP	B	85	7.134	43.501	11.551	1.00	32.67	C
ATOM	1503	C	ASP	B	85	7.527	44.753	12.304	1.00	31.61	C
ATOM	1504	O	ASP	B	85	7.290	45.876	11.852	1.00	30.78	O
ATOM	1505	CB	ASP	B	85	5.689	43.092	11.967	1.00	36.31	C

Figure 8-36

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ATOM   1506  CG  ASP B  85       4.984  42.012  11.146  1.00 36.50           C
ATOM   1507  OD1 ASP B  85       5.491  41.708  10.065  1.00 34.52           O
ATOM   1508  OD2 ASP B  85       3.945  41.485  11.574  1.00 37.36           O
ATOM   1509  N   LEU B  86       8.151  44.567  13.473  1.00 31.94           N
ATOM   1510  CA  LEU B  86       8.695  45.686  14.241  1.00 29.00           C
ATOM   1511  C   LEU B  86       9.945  46.335  13.646  1.00 27.01           C
ATOM   1512  O   LEU B  86      10.158  47.536  13.788  1.00 25.07           O
ATOM   1513  CB  LEU B  86       8.888  45.242  15.703  1.00 29.72           C
ATOM   1514  CG  LEU B  86       7.630  44.973  16.544  1.00 29.69           C
ATOM   1515  CD1 LEU B  86       7.934  44.246  17.825  1.00 29.68           C
ATOM   1516  CD2 LEU B  86       6.938  46.265  16.914  1.00 29.39           C
ATOM   1517  N   VAL B  87      10.774  45.550  12.962  1.00 26.28           N
ATOM   1518  CA  VAL B  87      11.895  46.068  12.214  1.00 29.27           C
ATOM   1519  C   VAL B  87      11.333  47.009  11.163  1.00 32.65           C
ATOM   1520  O   VAL B  87      11.721  48.175  11.164  1.00 35.43           O
ATOM   1521  CB  VAL B  87      12.725  44.966  11.523  1.00 28.93           C
ATOM   1522  CG1 VAL B  87      13.789  45.570  10.630  1.00 25.59           C
ATOM   1523  CG2 VAL B  87      13.417  44.036  12.521  1.00 30.50           C
ATOM   1524  N   GLU B  88      10.392  46.534  10.325  1.00 34.28           N
ATOM   1525  CA  GLU B  88       9.820  47.291   9.217  1.00 34.18           C
ATOM   1526  C   GLU B  88       9.201  48.582   9.702  1.00 34.90           C
ATOM   1527  O   GLU B  88       9.505  49.640   9.178  1.00 35.08           O
ATOM   1528  CB  GLU B  88       8.789  46.446   8.468  1.00 34.62           C
ATOM   1529  CG  GLU B  88       9.361  45.233   7.725  1.00 35.13           C
ATOM   1530  CD  GLU B  88       8.360  44.218   7.145  1.00 37.81           C
ATOM   1531  OE1 GLU B  88       7.241  44.088   7.653  1.00 39.42           O
ATOM   1532  OE2 GLU B  88       8.696  43.539   6.176  1.00 38.59           O
ATOM   1533  N   CYS B  89       8.402  48.520  10.754  1.00 37.74           N
ATOM   1534  CA  CYS B  89       7.803  49.680  11.378  1.00 41.43           C
ATOM   1535  C   CYS B  89       8.798  50.685  11.934  1.00 43.62           C
ATOM   1536  O   CYS B  89       8.578  51.896  11.896  1.00 44.63           O
ATOM   1537  CB  CYS B  89       6.875  49.166  12.472  1.00 43.51           C
ATOM   1538  SG  CYS B  89       6.538  50.326  13.821  1.00 52.54           S
ATOM   1539  N   VAL B  90       9.907  50.205  12.473  1.00 45.45           N
ATOM   1540  CA  VAL B  90      10.919  51.096  13.007  1.00 48.36           C
ATOM   1541  C   VAL B  90      11.787  51.723  11.909  1.00 49.57           C
ATOM   1542  O   VAL B  90      12.399  52.768  12.121  1.00 50.61           O
ATOM   1543  CB  VAL B  90      11.681  50.331  14.107  1.00 48.77           C
ATOM   1544  CG1 VAL B  90      12.903  51.039  14.582  1.00 51.24           C
ATOM   1545  CG2 VAL B  90      10.793  50.256  15.316  1.00 48.76           C
ATOM   1546  N   LYS B  91      11.834  51.181  10.695  1.00 50.84           N
ATOM   1547  CA  LYS B  91      12.492  51.870   9.600  1.00 52.46           C
ATOM   1548  C   LYS B  91      11.615  52.881   8.847  1.00 53.71           C
ATOM   1549  O   LYS B  91      12.139  53.730   8.127  1.00 52.07           O
ATOM   1550  CB  LYS B  91      13.135  50.840   8.721  1.00 54.00           C
ATOM   1551  CG  LYS B  91      14.290  50.209   9.508  1.00 59.12           C
ATOM   1552  CD  LYS B  91      14.955  49.089   8.690  1.00 63.16           C
ATOM   1553  CE  LYS B  91      16.176  48.420   9.367  1.00 66.55           C
ATOM   1554  NZ  LYS B  91      16.631  47.252   8.605  1.00 68.43           N
ATOM   1555  N   GLU B  92      10.283  52.858   9.066  1.00 56.63           N
ATOM   1556  CA  GLU B  92       9.333  53.861   8.565  1.00 59.16           C
ATOM   1557  C   GLU B  92       9.366  55.130   9.381  1.00 60.82           C
ATOM   1558  O   GLU B  92       9.635  56.189   8.802  1.00 61.59           O
ATOM   1559  CB  GLU B  92       7.852  53.434   8.599  1.00 60.60           C
ATOM   1560  CG  GLU B  92       7.388  52.228   7.784  1.00 63.20           C
ATOM   1561  CD  GLU B  92       7.621  52.275   6.273  1.00 66.00           C
ATOM   1562  OE1 GLU B  92       7.843  53.369   5.709  1.00 65.65           O
ATOM   1563  OE2 GLU B  92       7.564  51.187   5.667  1.00 67.41           O
ATOM   1564  N   ASN B  93       9.061  54.977  10.698  1.00 62.57           N
ATOM   1565  CA  ASN B  93       9.063  56.041  11.714  1.00 64.84           C
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Figure 8-37

ATOM	1566	C	ASN	B	93	10.247	56.971	11.593	1.00	65.46	C
ATOM	1567	O	ASN	B	93	11.368	56.721	12.018	1.00	65.03	O
ATOM	1568	CB	ASN	B	93	9.069	55.511	13.153	1.00	63.55	C
ATOM	1569	N	SER	B	94	9.868	58.041	10.904	1.00	68.52	N
ATOM	1570	CA	SER	B	94	10.773	58.985	10.254	1.00	70.87	C
ATOM	1571	C	SER	B	94	11.391	60.076	11.141	1.00	71.17	C
ATOM	1572	O	SER	B	94	12.292	60.821	10.689	1.00	72.46	O
ATOM	1573	CB	SER	B	94	10.028	59.573	9.039	1.00	71.38	C
ATOM	1574	OG	SER	B	94	8.711	60.001	9.407	1.00	73.36	O
ATOM	1575	N	SER	B	95	10.923	60.135	12.415	1.00	68.97	N
ATOM	1576	CA	SER	B	95	11.564	60.953	13.424	1.00	68.06	C
ATOM	1577	C	SER	B	95	13.040	60.572	13.473	1.00	67.28	C
ATOM	1578	O	SER	B	95	13.457	59.458	13.839	1.00	64.89	O
ATOM	1579	CB	SER	B	95	10.932	60.795	14.794	1.00	68.06	C
ATOM	1580	OG	SER	B	95	11.441	61.800	15.670	1.00	69.36	O
ATOM	1581	N	LYS	B	96	13.755	61.565	12.916	1.00	66.92	N
ATOM	1582	CA	LYS	B	96	15.199	61.518	12.771	1.00	67.27	C
ATOM	1583	C	LYS	B	96	15.848	60.974	14.056	1.00	66.10	C
ATOM	1584	O	LYS	B	96	16.615	59.996	14.014	1.00	64.46	O
ATOM	1585	CB	LYS	B	96	15.699	62.948	12.478	1.00	67.07	C
ATOM	1586	N	ASP	B	97	15.289	61.560	15.147	1.00	64.54	N
ATOM	1587	CA	ASP	B	97	15.657	61.369	16.562	1.00	62.82	C
ATOM	1588	C	ASP	B	97	15.739	59.968	17.239	1.00	60.00	C
ATOM	1589	O	ASP	B	97	16.792	59.674	17.852	1.00	59.90	O
ATOM	1590	CB	ASP	B	97	14.689	62.230	17.394	1.00	63.85	C
ATOM	1591	N	LEU	B	98	14.638	59.137	17.174	1.00	53.67	N
ATOM	1592	CA	LEU	B	98	14.641	57.690	17.447	1.00	44.35	C
ATOM	1593	C	LEU	B	98	15.837	57.135	16.728	1.00	40.32	C
ATOM	1594	O	LEU	B	98	15.868	57.109	15.497	1.00	40.10	O
ATOM	1595	CB	LEU	B	98	13.389	56.996	16.916	1.00	41.21	C
ATOM	1596	CG	LEU	B	98	13.251	55.479	17.095	1.00	40.48	C
ATOM	1597	CD1	LEU	B	98	11.904	55.030	17.695	1.00	39.61	C
ATOM	1598	CD2	LEU	B	98	13.519	54.787	15.784	1.00	37.90	C
ATOM	1599	N	LYS	B	99	16.815	56.840	17.593	1.00	36.84	N
ATOM	1600	CA	LYS	B	99	18.171	56.457	17.229	1.00	35.08	C
ATOM	1601	C	LYS	B	99	18.141	55.218	16.365	1.00	34.40	C
ATOM	1602	O	LYS	B	99	17.600	54.164	16.712	1.00	34.91	O
ATOM	1603	CB	LYS	B	99	19.028	56.193	18.485	1.00	35.16	C
ATOM	1604	CG	LYS	B	99	20.550	56.058	18.286	1.00	37.24	C
ATOM	1605	CD	LYS	B	99	21.314	55.641	19.556	1.00	36.33	C
ATOM	1606	CE	LYS	B	99	22.817	55.994	19.594	1.00	38.98	C
ATOM	1607	NZ	LYS	B	99	23.617	55.657	18.428	1.00	38.67	N
ATOM	1608	N	LYS	B	100	18.689	55.387	15.174	1.00	34.28	N
ATOM	1609	CA	LYS	B	100	18.726	54.285	14.232	1.00	34.35	C
ATOM	1610	C	LYS	B	100	20.147	53.964	13.811	1.00	31.26	C
ATOM	1611	O	LYS	B	100	20.368	52.917	13.224	1.00	32.09	O
ATOM	1612	CB	LYS	B	100	17.832	54.592	13.044	1.00	36.01	C
ATOM	1613	CG	LYS	B	100	16.335	54.635	13.349	1.00	38.72	C
ATOM	1614	CD	LYS	B	100	15.782	55.851	12.617	1.00	43.22	C
ATOM	1615	CE	LYS	B	100	14.290	55.723	12.370	1.00	43.50	C
ATOM	1616	NZ	LYS	B	100	13.982	55.990	10.969	1.00	43.57	N
ATOM	1617	N	SER	B	101	21.120	54.814	14.159	1.00	29.00	N
ATOM	1618	CA	SER	B	101	22.529	54.614	13.871	1.00	28.55	C
ATOM	1619	C	SER	B	101	23.351	54.047	15.032	1.00	28.24	C
ATOM	1620	O	SER	B	101	23.732	54.783	15.943	1.00	31.98	O
ATOM	1621	CB	SER	B	101	23.049	55.977	13.473	1.00	27.88	C
ATOM	1622	OG	SER	B	101	24.459	55.979	13.457	1.00	27.09	O
ATOM	1623	N	PHE	B	102	23.680	52.766	15.077	1.00	27.56	N
ATOM	1624	CA	PHE	B	102	24.364	52.184	16.230	1.00	27.12	C
ATOM	1625	C	PHE	B	102	25.620	51.495	15.755	1.00	28.99	C

Figure 8-38

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ATOM   1626  O   PHE B 102      25.613  51.001  14.627  1.00 28.31           O
ATOM   1627  CB  PHE B 102      23.538  51.127  16.945  1.00 22.35           C
ATOM   1628  CG  PHE B 102      22.247  51.672  17.462  1.00 20.73           C
ATOM   1629  CD1 PHE B 102      21.206  51.877  16.608  1.00 22.70           C
ATOM   1630  CD2 PHE B 102      22.105  51.932  18.801  1.00 24.01           C
ATOM   1631  CE1 PHE B 102      20.007  52.325  17.098  1.00 23.86           C
ATOM   1632  CE2 PHE B 102      20.892  52.343  19.295  1.00 23.54           C
ATOM   1633  CZ  PHE B 102      19.837  52.536  18.435  1.00 23.17           C
ATOM   1634  N   LYS B 103      26.691  51.459  16.575  1.00 30.21           N
ATOM   1635  CA  LYS B 103      27.823  50.595  16.284  1.00 30.86           C
ATOM   1636  C   LYS B 103      27.374  49.171  16.550  1.00 32.14           C
ATOM   1637  O   LYS B 103      26.583  48.957  17.472  1.00 33.74           O
ATOM   1638  CB  LYS B 103      28.965  50.952  17.200  1.00 32.77           C
ATOM   1639  N   SER B 104      27.788  48.202  15.720  1.00 32.95           N
ATOM   1640  CA  SER B 104      27.284  46.825  15.805  1.00 33.85           C
ATOM   1641  C   SER B 104      27.695  46.249  17.145  1.00 31.14           C
ATOM   1642  O   SER B 104      28.891  46.121  17.418  1.00 32.16           O
ATOM   1643  CB  SER B 104      27.812  45.908  14.692  1.00 36.29           C
ATOM   1644  OG  SER B 104      28.690  46.589  13.784  1.00 44.97           O
ATOM   1645  N   PRO B 105      26.737  45.950  18.023  1.00 28.62           N
ATOM   1646  CA  PRO B 105      27.026  45.601  19.393  1.00 27.39           C
ATOM   1647  C   PRO B 105      27.816  44.315  19.472  1.00 26.85           C
ATOM   1648  O   PRO B 105      27.947  43.532  18.527  1.00 29.04           O
ATOM   1649  CB  PRO B 105      25.668  45.476  19.982  1.00 26.67           C
ATOM   1650  CG  PRO B 105      24.803  46.313  19.104  1.00 26.85           C
ATOM   1651  CD  PRO B 105      25.308  45.910  17.747  1.00 26.48           C
ATOM   1652  N   GLU B 106      28.426  44.160  20.628  1.00 27.12           N
ATOM   1653  CA  GLU B 106      29.240  42.982  20.897  1.00 27.97           C
ATOM   1654  C   GLU B 106      28.299  41.806  21.172  1.00 25.13           C
ATOM   1655  O   GLU B 106      27.294  41.966  21.870  1.00 21.99           O
ATOM   1656  CB  GLU B 106      30.140  43.258  22.105  1.00 30.05           C
ATOM   1657  CG  GLU B 106      31.418  42.451  22.220  1.00 35.47           C
ATOM   1658  CD  GLU B 106      32.045  42.483  23.613  1.00 40.01           C
ATOM   1659  OE1 GLU B 106      32.162  43.570  24.198  1.00 41.10           O
ATOM   1660  OE2 GLU B 106      32.431  41.409  24.102  1.00 42.35           O
ATOM   1661  N   PRO B 107      28.564  40.640  20.578  1.00 23.74           N
ATOM   1662  CA  PRO B 107      27.806  39.423  20.817  1.00 24.07           C
ATOM   1663  C   PRO B 107      27.906  38.967  22.264  1.00 22.95           C
ATOM   1664  O   PRO B 107      28.989  38.920  22.832  1.00 24.47           O
ATOM   1665  CB  PRO B 107      28.437  38.439  19.837  1.00 24.75           C
ATOM   1666  CG  PRO B 107      28.949  39.309  18.715  1.00 25.17           C
ATOM   1667  CD  PRO B 107      29.556  40.448  19.512  1.00 24.46           C
ATOM   1668  N   ARG B 108      26.765  38.677  22.884  1.00 22.39           N
ATOM   1669  CA  ARG B 108      26.684  38.164  24.239  1.00 20.57           C
ATOM   1670  C   ARG B 108      25.904  36.865  24.227  1.00 17.43           C
ATOM   1671  O   ARG B 108      24.954  36.685  23.488  1.00 17.22           O
ATOM   1672  CB  ARG B 108      26.064  39.155  25.256  1.00 20.10           C
ATOM   1673  CG  ARG B 108      27.007  40.157  25.848  1.00 21.68           C
ATOM   1674  CD  ARG B 108      26.321  41.144  26.778  1.00 25.69           C
ATOM   1675  NE  ARG B 108      25.859  40.576  28.047  1.00 27.65           N
ATOM   1676  CZ  ARG B 108      25.517  41.345  29.084  1.00 26.15           C
ATOM   1677  NH1 ARG B 108      25.637  42.653  29.004  1.00 26.98           N
ATOM   1678  NH2 ARG B 108      25.031  40.819  30.217  1.00 27.28           N
ATOM   1679  N   LEU B 109      26.320  35.964  25.078  1.00 16.44           N
ATOM   1680  CA  LEU B 109      25.649  34.700  25.242  1.00 19.58           C
ATOM   1681  C   LEU B 109      24.667  34.827  26.384  1.00 19.57           C
ATOM   1682  O   LEU B 109      24.963  35.423  27.418  1.00 21.90           O
ATOM   1683  CB  LEU B 109      26.626  33.555  25.533  1.00 18.89           C
ATOM   1684  CG  LEU B 109      27.661  33.129  24.491  1.00 20.14           C
ATOM   1685  CD1 LEU B 109      28.673  32.188  25.119  1.00 18.71           C
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Figure 8-39

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ATOM   1686  CD2 LEU B 109      26.985  32.436  23.316  1.00 22.74           C
ATOM   1687  N   PHE B 110      23.477  34.293  26.119  1.00 19.30           N
ATOM   1688  CA  PHE B 110      22.372  34.322  27.050  1.00 18.85           C
ATOM   1689  C   PHE B 110      21.748  32.939  27.188  1.00 19.38           C
ATOM   1690  O   PHE B 110      21.676  32.205  26.207  1.00 18.43           O
ATOM   1691  CB  PHE B 110      21.312  35.298  26.553  1.00 17.38           C
ATOM   1692  CG  PHE B 110      21.743  36.756  26.567  1.00 19.20           C
ATOM   1693  CD1 PHE B 110      21.733  37.487  27.744  1.00 20.10           C
ATOM   1694  CD2 PHE B 110      22.198  37.350  25.408  1.00 19.07           C
ATOM   1695  CE1 PHE B 110      22.211  38.788  27.755  1.00 19.86           C
ATOM   1696  CE2 PHE B 110      22.643  38.650  25.436  1.00 15.79           C
ATOM   1697  CZ  PHE B 110      22.659  39.367  26.596  1.00 17.86           C
ATOM   1698  N   THR B 111      21.246  32.547  28.376  1.00 18.40           N
ATOM   1699  CA  THR B 111      20.431  31.336  28.505  1.00 14.95           C
ATOM   1700  C   THR B 111      19.077  31.537  27.823  1.00 14.86           C
ATOM   1701  O   THR B 111      18.720  32.705  27.696  1.00 18.62           O
ATOM   1702  CB  THR B 111      20.254  30.986  30.016  1.00 10.83           C
ATOM   1703  OG1 THR B 111      19.440  32.008  30.536  1.00 14.68           O
ATOM   1704  CG2 THR B 111      21.520  31.006  30.845  1.00 11.33           C
ATOM   1705  N   PRO B 112      18.205  30.602  27.418  1.00 14.14           N
ATOM   1706  CA  PRO B 112      16.903  30.899  26.832  1.00 12.85           C
ATOM   1707  C   PRO B 112      16.055  31.789  27.714  1.00 15.00           C
ATOM   1708  O   PRO B 112      15.351  32.679  27.268  1.00 16.67           O
ATOM   1709  CB  PRO B 112      16.297  29.536  26.730  1.00 13.18           C
ATOM   1710  CG  PRO B 112      17.459  28.689  26.406  1.00 11.71           C
ATOM   1711  CD  PRO B 112      18.482  29.179  27.402  1.00 12.63           C
ATOM   1712  N   GLU B 113      16.103  31.597  29.015  1.00 17.42           N
ATOM   1713  CA  GLU B 113      15.375  32.431  29.945  1.00 19.68           C
ATOM   1714  C   GLU B 113      15.802  33.888  29.901  1.00 18.59           C
ATOM   1715  O   GLU B 113      14.931  34.751  29.885  1.00 21.48           O
ATOM   1716  CB  GLU B 113      15.546  31.841  31.328  1.00 22.92           C
ATOM   1717  CG  GLU B 113      14.984  32.707  32.439  1.00 32.95           C
ATOM   1718  CD  GLU B 113      15.763  32.704  33.770  1.00 39.93           C
ATOM   1719  OE1 GLU B 113      16.869  33.281  33.900  1.00 41.39           O
ATOM   1720  OE2 GLU B 113      15.193  32.144  34.712  1.00 44.90           O
ATOM   1721  N   GLU B 114      17.096  34.210  29.885  1.00 18.49           N
ATOM   1722  CA  GLU B 114      17.601  35.576  29.760  1.00 17.43           C
ATOM   1723  C   GLU B 114      17.321  36.289  28.451  1.00 16.60           C
ATOM   1724  O   GLU B 114      16.910  37.449  28.404  1.00 19.48           O
ATOM   1725  CB  GLU B 114      19.090  35.543  29.980  1.00 19.55           C
ATOM   1726  CG  GLU B 114      19.486  35.319  31.442  1.00 23.40           C
ATOM   1727  CD  GLU B 114      20.962  35.034  31.718  1.00 25.98           C
ATOM   1728  OE1 GLU B 114      21.730  34.826  30.765  1.00 25.41           O
ATOM   1729  OE2 GLU B 114      21.322  34.982  32.906  1.00 28.77           O
ATOM   1730  N   PHE B 115      17.507  35.551  27.379  1.00 14.86           N
ATOM   1731  CA  PHE B 115      17.212  35.998  26.023  1.00 15.76           C
ATOM   1732  C   PHE B 115      15.776  36.422  25.843  1.00 14.74           C
ATOM   1733  O   PHE B 115      15.474  37.469  25.295  1.00 16.04           O
ATOM   1734  CB  PHE B 115      17.513  34.865  25.012  1.00 14.37           C
ATOM   1735  CG  PHE B 115      17.384  35.323  23.572  1.00 16.76           C
ATOM   1736  CD1 PHE B 115      18.400  36.062  22.990  1.00 15.08           C
ATOM   1737  CD2 PHE B 115      16.217  35.063  22.881  1.00 16.51           C
ATOM   1738  CE1 PHE B 115      18.169  36.611  21.755  1.00 15.92           C
ATOM   1739  CE2 PHE B 115      16.024  35.579  21.619  1.00 13.36           C
ATOM   1740  CZ  PHE B 115      16.994  36.364  21.079  1.00 14.28           C
ATOM   1741  N   PHE B 116      14.897  35.549  26.284  1.00 15.61           N
ATOM   1742  CA  PHE B 116      13.497  35.810  26.150  1.00 15.94           C
ATOM   1743  C   PHE B 116      12.918  36.798  27.125  1.00 16.92           C
ATOM   1744  O   PHE B 116      11.842  37.326  26.862  1.00 18.97           O
ATOM   1745  CB  PHE B 116      12.759  34.499  26.111  1.00 16.90           C
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Figure 8-40

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ATOM   1746  CG  PHE B 116      12.962  33.796  24.776  1.00 16.87           C
ATOM   1747  CD1 PHE B 116      12.315  34.278  23.639  1.00 16.00           C
ATOM   1748  CD2 PHE B 116      13.830  32.714  24.689  1.00 17.13           C
ATOM   1749  CE1 PHE B 116      12.558  33.654  22.429  1.00 17.64           C
ATOM   1750  CE2 PHE B 116      14.079  32.114  23.482  1.00 16.31           C
ATOM   1751  CZ  PHE B 116      13.427  32.582  22.349  1.00 17.77           C
ATOM   1752  N   ARG B 117      13.629  37.094  28.208  1.00 17.01           N
ATOM   1753  CA  ARG B 117      13.292  38.189  29.085  1.00 18.94           C
ATOM   1754  C   ARG B 117      13.636  39.492  28.388  1.00 20.76           C
ATOM   1755  O   ARG B 117      12.988  40.526  28.561  1.00 21.80           O
ATOM   1756  CB  ARG B 117      14.124  38.043  30.361  1.00 22.28           C
ATOM   1757  CG  ARG B 117      13.889  39.003  31.538  1.00 29.21           C
ATOM   1758  CD  ARG B 117      13.292  38.359  32.834  1.00 35.23           C
ATOM   1759  NE  ARG B 117      14.094  37.253  33.357  1.00 37.19           N
ATOM   1760  CZ  ARG B 117      15.408  37.373  33.616  1.00 42.10           C
ATOM   1761  NH1 ARG B 117      16.023  38.568  33.647  1.00 45.58           N
ATOM   1762  NH2 ARG B 117      16.151  36.268  33.794  1.00 43.18           N
ATOM   1763  N   ILE B 118      14.709  39.453  27.596  1.00 20.97           N
ATOM   1764  CA  ILE B 118      15.078  40.588  26.807  1.00 18.77           C
ATOM   1765  C   ILE B 118      14.103  40.799  25.662  1.00 20.54           C
ATOM   1766  O   ILE B 118      13.592  41.896  25.487  1.00 20.49           O
ATOM   1767  CB  ILE B 118      16.498  40.364  26.385  1.00 16.96           C
ATOM   1768  CG1 ILE B 118      17.377  40.504  27.587  1.00 17.82           C
ATOM   1769  CG2 ILE B 118      16.892  41.347  25.310  1.00 15.77           C
ATOM   1770  CD1 ILE B 118      18.851  40.271  27.253  1.00 14.00           C
ATOM   1771  N   PHE B 119      13.817  39.736  24.922  1.00 22.16           N
ATOM   1772  CA  PHE B 119      12.840  39.717  23.864  1.00 23.96           C
ATOM   1773  C   PHE B 119      11.528  40.271  24.356  1.00 26.51           C
ATOM   1774  O   PHE B 119      10.934  41.093  23.674  1.00 29.24           O
ATOM   1775  CB  PHE B 119      12.660  38.299  23.364  1.00 22.84           C
ATOM   1776  CG  PHE B 119      11.555  38.173  22.327  1.00 24.88           C
ATOM   1777  CD1 PHE B 119      11.811  38.512  21.006  1.00 25.69           C
ATOM   1778  CD2 PHE B 119      10.271  37.803  22.727  1.00 24.94           C
ATOM   1779  CE1 PHE B 119      10.748  38.539  20.122  1.00 25.07           C
ATOM   1780  CE2 PHE B 119       9.216  37.831  21.844  1.00 24.69           C
ATOM   1781  CZ  PHE B 119       9.465  38.212  20.539  1.00 25.22           C
ATOM   1782  N   ASN B 120      11.076  39.898  25.540  1.00 29.22           N
ATOM   1783  CA  ASN B 120       9.863  40.470  26.094  1.00 31.04           C
ATOM   1784  C   ASN B 120       9.953  41.939  26.499  1.00 32.79           C
ATOM   1785  O   ASN B 120       9.018  42.684  26.204  1.00 34.41           O
ATOM   1786  CB  ASN B 120       9.343  39.640  27.253  1.00 29.44           C
ATOM   1787  CG  ASN B 120       8.856  38.301  26.738  1.00 33.04           C
ATOM   1788  OD1 ASN B 120       8.264  38.216  25.651  1.00 32.93           O
ATOM   1789  ND2 ASN B 120       9.110  37.237  27.508  1.00 31.91           N
ATOM   1790  N   ARG B 121      11.018  42.436  27.140  1.00 32.47           N
ATOM   1791  CA  ARG B 121      11.117  43.849  27.465  1.00 30.92           C
ATOM   1792  C   ARG B 121      11.067  44.709  26.204  1.00 29.78           C
ATOM   1793  O   ARG B 121      10.444  45.760  26.207  1.00 28.95           O
ATOM   1794  CB  ARG B 121      12.391  44.075  28.271  1.00 33.61           C
ATOM   1795  CG  ARG B 121      12.655  45.523  28.664  1.00 41.90           C
ATOM   1796  CD  ARG B 121      11.463  46.261  29.336  1.00 48.78           C
ATOM   1797  NE  ARG B 121      11.048  47.453  28.567  1.00 55.93           N
ATOM   1798  CZ  ARG B 121      11.568  48.694  28.762  1.00 59.13           C
ATOM   1799  NH1 ARG B 121      12.543  48.894  29.659  1.00 60.86           N
ATOM   1800  NH2 ARG B 121      11.124  49.767  28.074  1.00 60.62           N
ATOM   1801  N   SER B 122      11.680  44.225  25.121  1.00 29.04           N
ATOM   1802  CA  SER B 122      11.818  44.920  23.854  1.00 27.66           C
ATOM   1803  C   SER B 122      10.512  45.006  23.126  1.00 29.01           C
ATOM   1804  O   SER B 122      10.198  46.085  22.634  1.00 30.77           O
ATOM   1805  CB  SER B 122      12.808  44.195  22.954  1.00 24.91           C
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Figure 8-41

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ATOM   1806  OG  SER B 122      14.125  44.237  23.464  1.00 21.03           O
ATOM   1807  N   ILE B 123       9.765  43.896  23.061  1.00 30.73           N
ATOM   1808  CA  ILE B 123       8.427  43.886  22.488  1.00 33.96           C
ATOM   1809  C   ILE B 123       7.513  44.857  23.232  1.00 38.09           C
ATOM   1810  O   ILE B 123       6.743  45.579  22.610  1.00 38.61           O
ATOM   1811  CB  ILE B 123       7.863  42.445  22.513  1.00 33.36           C
ATOM   1812  CG1 ILE B 123       8.567  41.492  21.559  1.00 33.77           C
ATOM   1813  CG2 ILE B 123       6.385  42.334  22.276  1.00 35.01           C
ATOM   1814  CD1 ILE B 123       8.539  41.729  20.058  1.00 31.14           C
ATOM   1815  N   ASP B 124       7.638  44.925  24.562  1.00 42.48           N
ATOM   1816  CA  ASP B 124       6.868  45.809  25.424  1.00 45.69           C
ATOM   1817  C   ASP B 124       7.347  47.237  25.404  1.00 45.68           C
ATOM   1818  O   ASP B 124       6.592  48.118  25.836  1.00 46.88           O
ATOM   1819  CB  ASP B 124       6.915  45.381  26.912  1.00 50.45           C
ATOM   1820  CG  ASP B 124       6.483  43.950  27.274  1.00 56.00           C
ATOM   1821  OD1 ASP B 124       5.766  43.310  26.481  1.00 61.21           O
ATOM   1822  OD2 ASP B 124       6.883  43.461  28.344  1.00 56.72           O
ATOM   1823  N   ALA B 125       8.599  47.461  24.970  1.00 46.60           N
ATOM   1824  CA  ALA B 125       9.190  48.801  24.903  1.00 47.64           C
ATOM   1825  C   ALA B 125       8.420  49.664  23.926  1.00 48.60           C
ATOM   1826  O   ALA B 125       8.412  50.882  24.081  1.00 48.65           O
ATOM   1827  CB  ALA B 125      10.643  48.781  24.422  1.00 46.01           C
ATOM   1828  N   PHE B 126       7.752  49.014  22.960  1.00 50.56           N
ATOM   1829  CA  PHE B 126       6.834  49.695  22.055  1.00 54.13           C
ATOM   1830  C   PHE B 126       5.525  50.182  22.688  1.00 57.79           C
ATOM   1831  O   PHE B 126       5.141  51.334  22.460  1.00 59.99           O
ATOM   1832  CB  PHE B 126       6.538  48.850  20.810  1.00 51.52           C
ATOM   1833  CG  PHE B 126       7.721  48.691  19.873  1.00 49.43           C
ATOM   1834  CD1 PHE B 126       8.650  47.685  20.086  1.00 48.93           C
ATOM   1835  CD2 PHE B 126       7.872  49.550  18.804  1.00 48.24           C
ATOM   1836  CE1 PHE B 126       9.721  47.531  19.226  1.00 47.28           C
ATOM   1837  CE2 PHE B 126       8.960  49.402  17.969  1.00 46.11           C
ATOM   1838  CZ  PHE B 126       9.882  48.401  18.174  1.00 45.91           C
ATOM   1839  N   LYS B 127       4.843  49.346  23.505  1.00 61.28           N
ATOM   1840  CA  LYS B 127       3.558  49.636  24.178  1.00 62.20           C
ATOM   1841  C   LYS B 127       3.454  50.906  25.026  1.00 62.03           C
ATOM   1842  O   LYS B 127       2.394  51.539  25.092  1.00 61.71           O
ATOM   1843  CB  LYS B 127       3.115  48.458  25.090  1.00 64.81           C
ATOM   1844  CG  LYS B 127       2.463  47.185  24.502  1.00 65.92           C
ATOM   1845  CD  LYS B 127       2.082  46.311  25.702  1.00 67.81           C
ATOM   1846  CE  LYS B 127       2.369  44.834  25.433  1.00 69.44           C
ATOM   1847  NZ  LYS B 127       2.594  44.129  26.691  1.00 68.14           N
ATOM   1848  N   ASP B 128       4.561  51.200  25.719  1.00 62.76           N
ATOM   1849  CA  ASP B 128       4.736  52.380  26.554  1.00 62.70           C
ATOM   1850  C   ASP B 128       5.573  53.412  25.794  1.00 63.56           C
ATOM   1851  O   ASP B 128       6.638  53.838  26.251  1.00 64.23           O
ATOM   1852  CB  ASP B 128       5.480  51.925  27.833  1.00 62.32           C
ATOM   1853  N   PHE B 129       5.128  53.802  24.587  1.00 64.47           N
ATOM   1854  CA  PHE B 129       5.813  54.828  23.801  1.00 65.58           C
ATOM   1855  C   PHE B 129       5.172  56.224  23.900  1.00 66.25           C
ATOM   1856  O   PHE B 129       4.145  56.473  23.258  1.00 67.17           O
ATOM   1857  CB  PHE B 129       5.971  54.368  22.338  1.00 64.56           C
ATOM   1858  CG  PHE B 129       7.424  54.230  21.907  1.00 63.61           C
ATOM   1859  CD1 PHE B 129       8.187  55.356  21.634  1.00 64.45           C
ATOM   1860  CD2 PHE B 129       7.979  52.977  21.775  1.00 62.93           C
ATOM   1861  CE1 PHE B 129       9.503  55.219  21.235  1.00 64.07           C
ATOM   1862  CE2 PHE B 129       9.291  52.837  21.378  1.00 63.56           C
ATOM   1863  CZ  PHE B 129      10.048  53.959  21.111  1.00 64.70           C
ATOM   1864  N   ASP B 137      17.272  62.584  24.623  1.00 55.18           N
ATOM   1865  CA  ASP B 137      18.560  63.025  24.106  1.00 54.96           C
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Figure 8-42

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ATOM   1866  C   ASP B 137      19.597  61.931  23.769  1.00 55.95           C
ATOM   1867  O   ASP B 137      20.291  62.026  22.743  1.00 55.11           O
ATOM   1868  CB  ASP B 137      19.180  63.952  25.136  1.00 53.99           C
ATOM   1869  N   CYS B 138      19.669  60.900  24.656  1.00 55.99           N
ATOM   1870  CA  CYS B 138      20.594  59.741  24.665  1.00 55.50           C
ATOM   1871  C   CYS B 138      22.065  59.964  25.031  1.00 55.10           C
ATOM   1872  O   CYS B 138      22.723  58.973  25.357  1.00 55.77           O
ATOM   1873  CB  CYS B 138      20.486  58.822  23.416  1.00 53.55           C
ATOM   1874  SG  CYS B 138      18.766  58.362  23.058  1.00 53.01           S
TER    1876      CYS B 138
ATOM   1877  N   ASN C  11      51.574  13.978  45.345  1.00 51.40           N
ATOM   1878  CA  ASN C  11      50.150  14.075  45.169  1.00 50.61           C
ATOM   1879  C   ASN C  11      49.636  15.080  46.231  1.00 51.75           C
ATOM   1880  O   ASN C  11      49.446  16.244  45.828  1.00 52.28           O
ATOM   1881  CB  ASN C  11      49.486  12.671  45.271  1.00 48.14           C
ATOM   1882  N   VAL C  12      49.577  14.664  47.548  1.00 49.74           N
ATOM   1883  CA  VAL C  12      48.941  15.269  48.771  1.00 46.17           C
ATOM   1884  C   VAL C  12      49.317  16.681  49.255  1.00 43.47           C
ATOM   1885  O   VAL C  12      48.526  17.397  49.868  1.00 42.02           O
ATOM   1886  CB  VAL C  12      49.032  14.271  50.044  1.00 47.02           C
ATOM   1887  CG1 VAL C  12      50.479  14.042  50.561  1.00 46.01           C
ATOM   1888  CG2 VAL C  12      48.129  14.662  51.233  1.00 44.78           C
ATOM   1889  N   LYS C  13      50.588  17.052  49.054  1.00 43.09           N
ATOM   1890  CA  LYS C  13      51.082  18.424  49.218  1.00 39.49           C
ATOM   1891  C   LYS C  13      50.370  19.321  48.180  1.00 36.49           C
ATOM   1892  O   LYS C  13      49.910  20.435  48.472  1.00 35.14           O
ATOM   1893  CB  LYS C  13      52.643  18.424  48.986  1.00 37.77           C
ATOM   1894  N   ASP C  14      50.231  18.776  46.951  1.00 33.25           N
ATOM   1895  CA  ASP C  14      49.522  19.456  45.898  1.00 27.29           C
ATOM   1896  C   ASP C  14      48.042  19.262  45.991  1.00 21.51           C
ATOM   1897  O   ASP C  14      47.408  20.205  45.602  1.00 20.53           O
ATOM   1898  CB  ASP C  14      50.101  19.142  44.565  1.00 31.10           C
ATOM   1899  CG  ASP C  14      51.439  19.856  44.288  1.00 35.88           C
ATOM   1900  OD1 ASP C  14      52.043  20.514  45.155  1.00 37.80           O
ATOM   1901  OD2 ASP C  14      51.890  19.755  43.143  1.00 37.19           O
ATOM   1902  N   VAL C  15      47.447  18.202  46.526  1.00 15.89           N
ATOM   1903  CA  VAL C  15      46.073  18.270  46.962  1.00 16.75           C
ATOM   1904  C   VAL C  15      45.796  19.433  47.938  1.00 17.73           C
ATOM   1905  O   VAL C  15      44.821  20.167  47.775  1.00 18.15           O
ATOM   1906  CB  VAL C  15      45.653  16.905  47.548  1.00 17.03           C
ATOM   1907  CG1 VAL C  15      44.266  16.920  48.161  1.00 15.16           C
ATOM   1908  CG2 VAL C  15      45.656  15.889  46.430  1.00 17.49           C
ATOM   1909  N   THR C  16      46.659  19.692  48.910  1.00 17.16           N
ATOM   1910  CA  THR C  16      46.513  20.824  49.806  1.00 16.51           C
ATOM   1911  C   THR C  16      46.660  22.151  49.096  1.00 15.07           C
ATOM   1912  O   THR C  16      45.901  23.049  49.418  1.00 16.99           O
ATOM   1913  CB  THR C  16      47.533  20.674  51.000  1.00 17.35           C
ATOM   1914  OG1 THR C  16      47.059  19.546  51.734  1.00 19.10           O
ATOM   1915  CG2 THR C  16      47.615  21.868  51.934  1.00 11.74           C
ATOM   1916  N   LYS C  17      47.562  22.381  48.160  1.00 13.81           N
ATOM   1917  CA  LYS C  17      47.496  23.602  47.390  1.00 15.88           C
ATOM   1918  C   LYS C  17      46.197  23.789  46.541  1.00 16.97           C
ATOM   1919  O   LYS C  17      45.608  24.877  46.465  1.00 17.88           O
ATOM   1920  CB  LYS C  17      48.702  23.598  46.505  1.00 18.13           C
ATOM   1921  CG  LYS C  17      50.006  23.615  47.257  1.00 21.24           C
ATOM   1922  CD  LYS C  17      51.103  23.441  46.198  1.00 24.88           C
ATOM   1923  CE  LYS C  17      52.486  23.537  46.798  1.00 28.59           C
ATOM   1924  NZ  LYS C  17      52.730  24.883  47.284  1.00 31.31           N
ATOM   1925  N   LEU C  18      45.682  22.736  45.880  1.00 14.39           N
ATOM   1926  CA  LEU C  18      44.454  22.764  45.149  1.00 11.22           C
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Figure 8-43

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ATOM   1927  C   LEU C  18      43.333  23.111  46.047  1.00 10.78           C
ATOM   1928  O   LEU C  18      42.612  24.032  45.691  1.00 16.08           O
ATOM   1929  CB  LEU C  18      44.129  21.412  44.609  1.00 12.69           C
ATOM   1930  CG  LEU C  18      42.973  21.312  43.632  1.00 15.70           C
ATOM   1931  CD1 LEU C  18      43.151  22.220  42.429  1.00  9.04           C
ATOM   1932  CD2 LEU C  18      42.864  19.875  43.248  1.00 15.11           C
ATOM   1933  N   VAL C  19      43.155  22.484  47.210  1.00 11.81           N
ATOM   1934  CA  VAL C  19      42.092  22.868  48.138  1.00 12.12           C
ATOM   1935  C   VAL C  19      42.159  24.359  48.569  1.00 13.12           C
ATOM   1936  O   VAL C  19      41.144  25.056  48.607  1.00 14.59           O
ATOM   1937  CB  VAL C  19      42.041  21.868  49.328  1.00 12.63           C
ATOM   1938  CG1 VAL C  19      40.984  22.267  50.328  1.00 11.49           C
ATOM   1939  CG2 VAL C  19      41.661  20.496  48.835  1.00 12.48           C
ATOM   1940  N   ALA C  20      43.362  24.909  48.821  1.00 13.02           N
ATOM   1941  CA  ALA C  20      43.532  26.278  49.252  1.00 11.77           C
ATOM   1942  C   ALA C  20      43.254  27.224  48.126  1.00 11.25           C
ATOM   1943  O   ALA C  20      42.888  28.357  48.344  1.00 14.74           O
ATOM   1944  CB  ALA C  20      44.975  26.452  49.635  1.00 10.68           C
ATOM   1945  N   ASN C  21      43.461  26.757  46.895  1.00 15.11           N
ATOM   1946  CA  ASN C  21      43.197  27.471  45.648  1.00 13.34           C
ATOM   1947  C   ASN C  21      41.898  27.107  44.949  1.00 13.09           C
ATOM   1948  O   ASN C  21      41.663  27.533  43.815  1.00 18.62           O
ATOM   1949  CB  ASN C  21      44.318  27.149  44.717  1.00 12.84           C
ATOM   1950  CG  ASN C  21      45.401  28.151  44.755  1.00 12.42           C
ATOM   1951  OD1 ASN C  21      45.277  29.229  45.315  1.00 14.66           O
ATOM   1952  ND2 ASN C  21      46.503  27.827  44.131  1.00 12.99           N
ATOM   1953  N   LEU C  22      41.041  26.311  45.536  1.00 12.25           N
ATOM   1954  CA  LEU C  22      39.691  26.194  45.063  1.00 12.28           C
ATOM   1955  C   LEU C  22      38.831  27.012  45.972  1.00 12.85           C
ATOM   1956  O   LEU C  22      39.216  27.109  47.126  1.00 17.11           O
ATOM   1957  CB  LEU C  22      39.202  24.755  45.039  1.00 10.06           C
ATOM   1958  CG  LEU C  22      39.745  23.906  43.936  1.00  9.08           C
ATOM   1959  CD1 LEU C  22      39.380  22.464  44.120  1.00  8.06           C
ATOM   1960  CD2 LEU C  22      39.124  24.394  42.666  1.00 11.26           C
ATOM   1961  N   PRO C  23      37.706  27.649  45.629  1.00 12.49           N
ATOM   1962  CA  PRO C  23      36.902  28.384  46.592  1.00 12.26           C
ATOM   1963  C   PRO C  23      36.214  27.457  47.604  1.00 13.42           C
ATOM   1964  O   PRO C  23      35.695  26.416  47.220  1.00 13.22           O
ATOM   1965  CB  PRO C  23      35.923  29.108  45.681  1.00 13.14           C
ATOM   1966  CG  PRO C  23      36.407  29.009  44.237  1.00  9.94           C
ATOM   1967  CD  PRO C  23      37.094  27.667  44.292  1.00 12.73           C
ATOM   1968  N   LYS C  24      36.216  27.796  48.898  1.00 13.54           N
ATOM   1969  CA  LYS C  24      35.515  27.039  49.919  1.00 17.03           C
ATOM   1970  C   LYS C  24      34.053  26.703  49.596  1.00 17.41           C
ATOM   1971  O   LYS C  24      33.500  25.693  50.011  1.00 15.96           O
ATOM   1972  CB  LYS C  24      35.591  27.845  51.228  1.00 17.76           C
ATOM   1973  CG  LYS C  24      36.918  27.585  51.896  1.00 22.90           C
ATOM   1974  CD  LYS C  24      37.423  28.782  52.700  1.00 24.73           C
ATOM   1975  CE  LYS C  24      38.893  28.608  53.191  1.00 25.32           C
ATOM   1976  NZ  LYS C  24      39.427  29.914  53.578  1.00 27.67           N
ATOM   1977  N   ASP C  25      33.380  27.526  48.807  1.00 20.45           N
ATOM   1978  CA  ASP C  25      31.969  27.349  48.579  1.00 20.93           C
ATOM   1979  C   ASP C  25      31.690  26.924  47.164  1.00 19.35           C
ATOM   1980  O   ASP C  25      30.617  27.146  46.603  1.00 21.38           O
ATOM   1981  CB  ASP C  25      31.316  28.665  48.909  1.00 23.07           C
ATOM   1982  CG  ASP C  25      31.726  29.820  48.014  1.00 28.48           C
ATOM   1983  OD1 ASP C  25      32.736  29.755  47.329  1.00 29.48           O
ATOM   1984  OD2 ASP C  25      31.018  30.829  48.006  1.00 35.37           O
ATOM   1985  N   TYR C  26      32.684  26.330  46.570  1.00 17.08           N
ATOM   1986  CA  TYR C  26      32.486  25.784  45.270  1.00 18.09           C
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Figure 8-44

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ATOM   1987  C   TYR C  26      32.066  24.352  45.473  1.00 20.16           C
ATOM   1988  O   TYR C  26      32.672  23.586  46.210  1.00 20.74           O
ATOM   1989  CB  TYR C  26      33.787  25.925  44.505  1.00 18.65           C
ATOM   1990  CG  TYR C  26      33.779  25.389  43.087  1.00 15.43           C
ATOM   1991  CD1 TYR C  26      32.863  25.870  42.180  1.00 14.28           C
ATOM   1992  CD2 TYR C  26      34.687  24.394  42.740  1.00 18.66           C
ATOM   1993  CE1 TYR C  26      32.828  25.305  40.916  1.00 18.89           C
ATOM   1994  CE2 TYR C  26      34.680  23.853  41.457  1.00 18.57           C
ATOM   1995  CZ  TYR C  26      33.736  24.325  40.567  1.00 17.94           C
ATOM   1996  OH  TYR C  26      33.702  23.844  39.293  1.00 20.05           O
HETATM 1997  N   MSE C  27      30.992  23.977  44.806  1.00 22.38           N
HETATM 1998  CA  MSE C  27      30.472  22.643  44.960  1.00 23.82           C
HETATM 1999  C   MSE C  27      30.902  21.790  43.796  1.00 23.07           C
HETATM 2000  O   MSE C  27      30.675  22.180  42.659  1.00 22.78           O
HETATM 2001  CB  MSE C  27      28.966  22.685  45.023  1.00 27.76           C
HETATM 2002  CG  MSE C  27      28.476  23.440  46.222  1.00 33.28           C
HETATM 2003  SE  MSE C  27      29.250  22.864  47.919  1.00 47.63          SE
HETATM 2004  CE  MSE C  27      28.807  24.413  48.975  1.00 42.81           C
ATOM   2005  N   ILE C  28      31.514  20.637  44.127  1.00 23.36           N
ATOM   2006  CA  ILE C  28      31.890  19.552  43.196  1.00 24.49           C
ATOM   2007  C   ILE C  28      30.924  18.334  43.195  1.00 25.21           C
ATOM   2008  O   ILE C  28      30.568  17.795  44.237  1.00 24.49           O
ATOM   2009  CB  ILE C  28      33.364  19.075  43.497  1.00 21.68           C
ATOM   2010  CG1 ILE C  28      34.379  20.215  43.453  1.00 19.99           C
ATOM   2011  CG2 ILE C  28      33.796  18.049  42.485  1.00 19.57           C
ATOM   2012  CD1 ILE C  28      35.761  19.859  43.991  1.00 18.85           C
ATOM   2013  N   THR C  29      30.508  17.846  42.017  1.00 26.46           N
ATOM   2014  CA  THR C  29      29.637  16.688  41.888  1.00 26.80           C
ATOM   2015  C   THR C  29      30.388  15.361  41.957  1.00 27.21           C
ATOM   2016  O   THR C  29      31.299  15.084  41.182  1.00 26.27           O
ATOM   2017  CB  THR C  29      28.824  16.736  40.580  1.00 25.22           C
ATOM   2018  OG1 THR C  29      28.137  17.962  40.566  1.00 28.05           O
ATOM   2019  CG2 THR C  29      27.773  15.659  40.545  1.00 26.26           C
ATOM   2020  N   LEU C  30      29.980  14.498  42.878  1.00 27.91           N
ATOM   2021  CA  LEU C  30      30.519  13.157  42.943  1.00 29.69           C
ATOM   2022  C   LEU C  30      29.354  12.189  43.168  1.00 31.34           C
ATOM   2023  O   LEU C  30      28.542  12.362  44.080  1.00 30.99           O
ATOM   2024  CB  LEU C  30      31.578  13.070  44.051  1.00 25.27           C
ATOM   2025  CG  LEU C  30      32.157  11.727  44.434  1.00 23.15           C
ATOM   2026  CD1 LEU C  30      32.879  11.106  43.274  1.00 22.85           C
ATOM   2027  CD2 LEU C  30      33.110  11.943  45.570  1.00 25.04           C
ATOM   2028  N   LYS C  31      29.246  11.172  42.300  1.00 34.65           N
ATOM   2029  CA  LYS C  31      28.335  10.045  42.513  1.00 36.49           C
ATOM   2030  C   LYS C  31      28.910   9.150  43.620  1.00 36.03           C
ATOM   2031  O   LYS C  31      29.741   8.287  43.370  1.00 36.42           O
ATOM   2032  CB  LYS C  31      28.121   9.241  41.218  1.00 36.56           C
ATOM   2033  CG  LYS C  31      27.475   9.966  40.056  1.00 39.42           C
ATOM   2034  CD  LYS C  31      26.867   8.902  39.121  1.00 47.68           C
ATOM   2035  CE  LYS C  31      25.930   9.427  37.990  1.00 51.31           C
ATOM   2036  NZ  LYS C  31      24.859   8.496  37.602  1.00 51.86           N
ATOM   2037  N   TYR C  32      28.514   9.411  44.868  1.00 38.89           N
ATOM   2038  CA  TYR C  32      29.122   8.846  46.081  1.00 40.86           C
ATOM   2039  C   TYR C  32      28.594   7.437  46.265  1.00 43.51           C
ATOM   2040  O   TYR C  32      27.425   7.204  45.953  1.00 45.02           O
ATOM   2041  CB  TYR C  32      28.707   9.747  47.229  1.00 37.67           C
ATOM   2042  CG  TYR C  32      29.138   9.317  48.610  1.00 41.48           C
ATOM   2043  CD1 TYR C  32      30.459   9.438  48.984  1.00 43.11           C
ATOM   2044  CD2 TYR C  32      28.190   8.877  49.536  1.00 43.18           C
ATOM   2045  CE1 TYR C  32      30.812   9.172  50.302  1.00 44.55           C
ATOM   2046  CE2 TYR C  32      28.542   8.584  50.847  1.00 44.09           C
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Figure 8-45

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ATOM   2047  CZ  TYR C  32      29.862   8.758  51.230  1.00 45.88           C
ATOM   2048  OH  TYR C  32      30.238   8.549  52.557  1.00 49.38           O
ATOM   2049  N   VAL C  33      29.391   6.459  46.718  1.00 46.10           N
ATOM   2050  CA  VAL C  33      28.866   5.097  46.885  1.00 48.63           C
ATOM   2051  C   VAL C  33      28.323   4.935  48.307  1.00 50.48           C
ATOM   2052  O   VAL C  33      29.088   5.086  49.265  1.00 49.75           O
ATOM   2053  CB  VAL C  33      29.900   4.000  46.501  1.00 49.02           C
ATOM   2054  CG1 VAL C  33      29.390   2.594  46.823  1.00 50.53           C
ATOM   2055  CG2 VAL C  33      30.216   4.072  45.014  1.00 47.63           C
ATOM   2056  N   PRO C  34      27.006   4.682  48.505  1.00 53.28           N
ATOM   2057  CA  PRO C  34      26.385   4.695  49.834  1.00 55.66           C
ATOM   2058  C   PRO C  34      27.121   3.734  50.767  1.00 58.89           C
ATOM   2059  O   PRO C  34      27.426   2.568  50.448  1.00 59.22           O
ATOM   2060  CB  PRO C  34      24.936   4.297  49.549  1.00 54.96           C
ATOM   2061  CG  PRO C  34      24.701   4.825  48.139  1.00 51.80           C
ATOM   2062  CD  PRO C  34      26.002   4.428  47.456  1.00 51.86           C
ATOM   2063  N   GLY C  35      27.545   4.399  51.850  1.00 60.51           N
ATOM   2064  CA  GLY C  35      28.272   3.744  52.925  1.00 62.88           C
ATOM   2065  C   GLY C  35      29.632   3.266  52.457  1.00 63.14           C
ATOM   2066  O   GLY C  35      29.852   2.077  52.214  1.00 64.01           O
HETATM 2067  N   MSE C  36      30.521   4.240  52.301  1.00 62.92           N
HETATM 2068  CA  MSE C  36      31.881   3.970  51.881  1.00 63.09           C
HETATM 2069  C   MSE C  36      32.945   4.485  52.836  1.00 64.77           C
HETATM 2070  O   MSE C  36      34.148   4.357  52.599  1.00 65.03           O
HETATM 2071  CB  MSE C  36      32.115   4.582  50.531  1.00 62.61           C
HETATM 2072  CG  MSE C  36      31.973   6.068  50.551  1.00 60.55           C
HETATM 2073  SE  MSE C  36      33.277   6.879  49.401  1.00 61.18          SE
HETATM 2074  CE  MSE C  36      34.541   7.346  50.777  1.00 55.15           C
ATOM   2075  N   ASP C  37      32.430   5.163  53.863  1.00 66.73           N
ATOM   2076  CA  ASP C  37      33.149   5.583  55.061  1.00 67.41           C
ATOM   2077  C   ASP C  37      33.215   4.481  56.132  1.00 66.85           C
ATOM   2078  O   ASP C  37      34.130   4.393  56.957  1.00 67.21           O
ATOM   2079  CB  ASP C  37      32.478   6.867  55.589  1.00 69.00           C
ATOM   2080  CG  ASP C  37      30.982   6.808  55.935  1.00 70.25           C
ATOM   2081  OD1 ASP C  37      30.143   6.538  55.061  1.00 69.81           O
ATOM   2082  OD2 ASP C  37      30.657   7.058  57.097  1.00 71.69           O
ATOM   2083  N   VAL C  38      32.224   3.593  56.068  1.00 65.94           N
ATOM   2084  CA  VAL C  38      32.091   2.461  56.960  1.00 64.55           C
ATOM   2085  C   VAL C  38      32.395   1.200  56.170  1.00 65.94           C
ATOM   2086  O   VAL C  38      33.340   0.521  56.584  1.00 68.33           O
ATOM   2087  CB  VAL C  38      30.694   2.475  57.631  1.00 63.05           C
ATOM   2088  CG1 VAL C  38      29.960   1.135  57.787  1.00 62.73           C
ATOM   2089  CG2 VAL C  38      30.915   3.097  58.990  1.00 61.39           C
ATOM   2090  N   LEU C  39      31.700   0.861  55.059  1.00 64.32           N
ATOM   2091  CA  LEU C  39      31.997  -0.365  54.328  1.00 63.23           C
ATOM   2092  C   LEU C  39      33.487  -0.412  53.952  1.00 62.57           C
ATOM   2093  O   LEU C  39      34.084   0.647  53.713  1.00 63.24           O
ATOM   2094  CB  LEU C  39      31.130  -0.449  53.078  1.00 62.74           C
ATOM   2095  N   PRO C  40      34.161  -1.578  54.006  1.00 61.57           N
ATOM   2096  CA  PRO C  40      35.608  -1.719  53.761  1.00 59.74           C
ATOM   2097  C   PRO C  40      36.009  -1.462  52.318  1.00 57.52           C
ATOM   2098  O   PRO C  40      35.183  -1.629  51.418  1.00 54.10           O
ATOM   2099  CB  PRO C  40      35.861  -3.170  54.123  1.00 60.55           C
ATOM   2100  CG  PRO C  40      34.550  -3.863  53.762  1.00 60.74           C
ATOM   2101  CD  PRO C  40      33.546  -2.868  54.329  1.00 61.16           C
ATOM   2102  N   SER C  41      37.282  -1.110  52.111  1.00 56.39           N
ATOM   2103  CA  SER C  41      37.779  -0.735  50.798  1.00 56.77           C
ATOM   2104  C   SER C  41      37.271  -1.553  49.602  1.00 56.41           C
ATOM   2105  O   SER C  41      36.627  -0.992  48.727  1.00 56.58           O
ATOM   2106  CB  SER C  41      39.292  -0.643  50.831  1.00 57.36           C
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Figure 8-46

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ATOM   2107  OG  SER C  41      39.964  -1.877  50.695  1.00 60.69           O
ATOM   2108  N   HIS C  42      37.404  -2.882  49.580  1.00 56.11           N
ATOM   2109  CA  HIS C  42      36.947  -3.739  48.482  1.00 56.80           C
ATOM   2110  C   HIS C  42      35.473  -3.664  48.079  1.00 56.34           C
ATOM   2111  O   HIS C  42      35.062  -4.139  47.007  1.00 55.64           O
ATOM   2112  CB  HIS C  42      37.301  -5.217  48.795  1.00 60.78           C
ATOM   2113  CG  HIS C  42      36.205  -6.095  49.445  1.00 63.24           C
ATOM   2114  ND1 HIS C  42      35.894  -6.211  50.736  1.00 63.50           N
ATOM   2115  CD2 HIS C  42      35.244  -6.788  48.711  1.00 63.78           C
ATOM   2116  CE1 HIS C  42      34.762  -6.882  50.802  1.00 64.65           C
ATOM   2117  NE2 HIS C  42      34.371  -7.201  49.584  1.00 64.49           N
ATOM   2118  N   CYS C  43      34.669  -3.175  49.027  1.00 56.27           N
ATOM   2119  CA  CYS C  43      33.239  -3.012  48.806  1.00 56.25           C
ATOM   2120  C   CYS C  43      32.953  -1.871  47.844  1.00 54.69           C
ATOM   2121  O   CYS C  43      32.104  -2.006  46.959  1.00 56.17           O
ATOM   2122  CB  CYS C  43      32.488  -2.787  50.120  1.00 57.47           C
ATOM   2123  SG  CYS C  43      31.647  -4.253  50.786  1.00 60.51           S
ATOM   2124  N   TRP C  44      33.695  -0.766  47.973  1.00 51.41           N
ATOM   2125  CA  TRP C  44      33.338   0.464  47.287  1.00 47.58           C
ATOM   2126  C   TRP C  44      34.349   0.946  46.300  1.00 46.08           C
ATOM   2127  O   TRP C  44      33.969   1.593  45.341  1.00 46.29           O
ATOM   2128  CB  TRP C  44      33.089   1.587  48.271  1.00 47.09           C
ATOM   2129  CG  TRP C  44      34.199   1.801  49.301  1.00 46.63           C
ATOM   2130  CD1 TRP C  44      34.221   1.046  50.444  1.00 47.77           C
ATOM   2131  CD2 TRP C  44      35.261   2.660  49.225  1.00 45.55           C
ATOM   2132  NE1 TRP C  44      35.307   1.419  51.078  1.00 47.46           N
ATOM   2133  CE2 TRP C  44      35.948   2.361  50.389  1.00 44.86           C
ATOM   2134  CE3 TRP C  44      35.723   3.640  48.403  1.00 42.70           C
ATOM   2135  CZ2 TRP C  44      37.122   2.956  50.754  1.00 43.79           C
ATOM   2136  CZ3 TRP C  44      36.886   4.263  48.782  1.00 43.82           C
ATOM   2137  CH2 TRP C  44      37.597   3.925  49.920  1.00 42.91           C
ATOM   2138  N   ILE C  45      35.615   0.635  46.539  1.00 45.14           N
ATOM   2139  CA  ILE C  45      36.735   1.252  45.851  1.00 47.08           C
ATOM   2140  C   ILE C  45      36.657   1.198  44.329  1.00 47.61           C
ATOM   2141  O   ILE C  45      36.955   2.157  43.619  1.00 48.87           O
ATOM   2142  CB  ILE C  45      38.085   0.681  46.427  1.00 47.91           C
ATOM   2143  CG1 ILE C  45      39.316   1.515  46.123  1.00 46.35           C
ATOM   2144  CG2 ILE C  45      38.420  -0.723  45.905  1.00 50.05           C
ATOM   2145  CD1 ILE C  45      39.180   2.995  46.462  1.00 43.72           C
ATOM   2146  N   SER C  46      36.158   0.077  43.850  1.00 47.61           N
ATOM   2147  CA  SER C  46      36.069  -0.245  42.437  1.00 48.09           C
ATOM   2148  C   SER C  46      35.166   0.685  41.595  1.00 47.26           C
ATOM   2149  O   SER C  46      35.598   1.186  40.555  1.00 46.49           O
ATOM   2150  CB  SER C  46      35.688  -1.728  42.427  1.00 50.90           C
ATOM   2151  OG  SER C  46      35.093  -2.219  43.664  1.00 54.24           O
ATOM   2152  N   GLU C  47      33.932   0.997  42.039  1.00 46.80           N
ATOM   2153  CA  GLU C  47      33.095   2.037  41.430  1.00 45.94           C
ATOM   2154  C   GLU C  47      33.599   3.449  41.776  1.00 43.82           C
ATOM   2155  O   GLU C  47      33.532   4.348  40.947  1.00 43.16           O
ATOM   2156  CB  GLU C  47      31.602   1.843  41.831  1.00 47.29           C
ATOM   2157  CG  GLU C  47      30.478   2.752  41.246  1.00 52.00           C
ATOM   2158  CD  GLU C  47      29.748   2.394  39.936  1.00 54.16           C
ATOM   2159  OE1 GLU C  47      28.894   1.494  39.926  1.00 57.21           O
ATOM   2160  OE2 GLU C  47      29.989   3.052  38.922  1.00 54.36           O
HETATM 2161  N   MSE C  48      34.170   3.670  42.967  1.00 43.01           N
HETATM 2162  CA  MSE C  48      34.601   4.979  43.448  1.00 40.77           C
HETATM 2163  C   MSE C  48      35.795   5.538  42.724  1.00 37.10           C
HETATM 2164  O   MSE C  48      35.799   6.739  42.563  1.00 39.16           O
HETATM 2165  CB  MSE C  48      34.926   4.968  44.927  1.00 43.83           C
HETATM 2166  CG  MSE C  48      34.667   6.334  45.551  1.00 49.60           C
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Figure 8-47

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HETATM 2167 SE   MSE C  48      32.809   6.850  45.340  1.00 57.46          SE
HETATM 2168  CE  MSE C  48      32.917   8.464  46.266  1.00 52.90           C
ATOM   2169  N   VAL C  49      36.793   4.773  42.266  1.00 34.29           N
ATOM   2170  CA  VAL C  49      37.855   5.271  41.388  1.00 30.22           C
ATOM   2171  C   VAL C  49      37.372   5.680  39.997  1.00 31.03           C
ATOM   2172  O   VAL C  49      37.936   6.572  39.365  1.00 30.17           O
ATOM   2173  CB  VAL C  49      39.021   4.288  41.268  1.00 27.65           C
ATOM   2174  CG1 VAL C  49      39.719   4.131  42.581  1.00 27.80           C
ATOM   2175  CG2 VAL C  49      38.591   2.924  40.828  1.00 27.38           C
ATOM   2176  N   VAL C  50      36.319   5.056  39.478  1.00 29.68           N
ATOM   2177  CA  VAL C  50      35.727   5.548  38.255  1.00 29.53           C
ATOM   2178  C   VAL C  50      34.932   6.806  38.559  1.00 28.57           C
ATOM   2179  O   VAL C  50      35.069   7.755  37.800  1.00 30.41           O
ATOM   2180  CB  VAL C  50      34.904   4.446  37.554  1.00 30.06           C
ATOM   2181  CG1 VAL C  50      34.026   4.900  36.371  1.00 28.50           C
ATOM   2182  CG2 VAL C  50      35.916   3.457  37.070  1.00 29.52           C
ATOM   2183  N   GLN C  51      34.147   6.917  39.639  1.00 28.05           N
ATOM   2184  CA  GLN C  51      33.421   8.148  39.945  1.00 27.55           C
ATOM   2185  C   GLN C  51      34.267   9.336  40.379  1.00 26.77           C
ATOM   2186  O   GLN C  51      33.957  10.480  40.061  1.00 27.78           O
ATOM   2187  CB  GLN C  51      32.276   7.962  40.944  1.00 27.95           C
ATOM   2188  CG  GLN C  51      31.142   7.029  40.503  1.00 31.66           C
ATOM   2189  CD  GLN C  51      30.518   7.274  39.121  1.00 35.14           C
ATOM   2190  OE1 GLN C  51      30.531   8.353  38.510  1.00 34.94           O
ATOM   2191  NE2 GLN C  51      29.945   6.214  38.566  1.00 36.11           N
ATOM   2192  N   LEU C  52      35.349   9.130  41.113  1.00 24.84           N
ATOM   2193  CA  LEU C  52      36.290  10.188  41.316  1.00 24.73           C
ATOM   2194  C   LEU C  52      36.914  10.560  40.004  1.00 25.82           C
ATOM   2195  O   LEU C  52      37.061  11.752  39.750  1.00 26.91           O
ATOM   2196  CB  LEU C  52      37.349   9.754  42.251  1.00 25.92           C
ATOM   2197  CG  LEU C  52      36.831   9.701  43.653  1.00 27.26           C
ATOM   2198  CD1 LEU C  52      37.880   9.090  44.510  1.00 27.86           C
ATOM   2199  CD2 LEU C  52      36.473  11.078  44.141  1.00 27.93           C
ATOM   2200  N   SER C  53      37.211   9.566  39.148  1.00 27.18           N
ATOM   2201  CA  SER C  53      37.788   9.790  37.838  1.00 24.69           C
ATOM   2202  C   SER C  53      36.859  10.558  36.918  1.00 26.00           C
ATOM   2203  O   SER C  53      37.336  11.388  36.166  1.00 26.97           O
ATOM   2204  CB  SER C  53      38.172   8.499  37.198  1.00 25.64           C
ATOM   2205  OG  SER C  53      38.902   8.772  36.019  1.00 24.45           O
ATOM   2206  N   ASP C  54      35.544  10.421  36.932  1.00 27.50           N
ATOM   2207  CA  ASP C  54      34.743  11.292  36.113  1.00 29.13           C
ATOM   2208  C   ASP C  54      34.719  12.679  36.663  1.00 27.20           C
ATOM   2209  O   ASP C  54      34.826  13.616  35.906  1.00 30.75           O
ATOM   2210  CB  ASP C  54      33.314  10.874  36.099  1.00 35.74           C
ATOM   2211  CG  ASP C  54      33.056   9.521  35.502  1.00 43.27           C
ATOM   2212  OD1 ASP C  54      33.871   9.016  34.694  1.00 44.80           O
ATOM   2213  OD2 ASP C  54      31.996   8.988  35.876  1.00 47.24           O
ATOM   2214  N   SER C  55      34.554  12.829  37.966  1.00 26.41           N
ATOM   2215  CA  SER C  55      34.470  14.119  38.610  1.00 23.34           C
ATOM   2216  C   SER C  55      35.676  14.964  38.382  1.00 19.99           C
ATOM   2217  O   SER C  55      35.544  16.157  38.175  1.00 20.42           O
ATOM   2218  CB  SER C  55      34.306  13.948  40.105  1.00 24.60           C
ATOM   2219  OG  SER C  55      33.079  13.321  40.431  1.00 24.29           O
ATOM   2220  N   LEU C  56      36.837  14.338  38.432  1.00 19.40           N
ATOM   2221  CA  LEU C  56      38.082  15.062  38.245  1.00 21.98           C
ATOM   2222  C   LEU C  56      38.333  15.488  36.797  1.00 23.22           C
ATOM   2223  O   LEU C  56      38.922  16.543  36.512  1.00 21.76           O
ATOM   2224  CB  LEU C  56      39.301  14.271  38.793  1.00 21.06           C
ATOM   2225  CG  LEU C  56      39.614  14.342  40.291  1.00 19.56           C
ATOM   2226  CD1 LEU C  56      40.647  13.313  40.678  1.00 18.16           C
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Figure 8-48

ATOM	2227	CD2	LEU	C	56	40.132	15.717	40.651	1.00	16.61	C
ATOM	2228	N	THR	C	57	37.873	14.624	35.881	1.00	25.77	N
ATOM	2229	CA	THR	C	57	37.991	14.906	34.462	1.00	28.23	C
ATOM	2230	C	THR	C	57	37.020	16.004	34.104	1.00	28.03	C
ATOM	2231	O	THR	C	57	37.390	16.908	33.364	1.00	31.55	O
ATOM	2232	CB	THR	C	57	37.813	13.669	33.596	1.00	30.08	C
ATOM	2233	OG1	THR	C	57	38.904	12.849	33.972	1.00	32.28	O
ATOM	2234	CG2	THR	C	57	38.044	13.945	32.109	1.00	33.98	C
ATOM	2235	N	ASP	C	58	35.831	16.009	34.675	1.00	26.77	N
ATOM	2236	CA	ASP	C	58	34.940	17.120	34.486	1.00	29.31	C
ATOM	2237	C	ASP	C	58	35.387	18.422	35.173	1.00	28.49	C
ATOM	2238	O	ASP	C	58	35.241	19.515	34.614	1.00	29.44	O
ATOM	2239	CB	ASP	C	58	33.489	16.679	34.870	1.00	36.00	C
ATOM	2240	CG	ASP	C	58	32.849	15.532	34.032	1.00	40.53	C
ATOM	2241	OD1	ASP	C	58	33.503	14.924	33.151	1.00	41.90	O
ATOM	2242	OD2	ASP	C	58	31.673	15.229	34.294	1.00	42.29	O
ATOM	2243	N	LEU	C	59	35.964	18.350	36.383	1.00	26.07	N
ATOM	2244	CA	LEU	C	59	36.486	19.508	37.074	1.00	21.52	C
ATOM	2245	C	LEU	C	59	37.611	20.115	36.285	1.00	19.04	C
ATOM	2246	O	LEU	C	59	37.748	21.317	36.312	1.00	20.31	O
ATOM	2247	CB	LEU	C	59	37.028	19.118	38.444	1.00	19.27	C
ATOM	2248	CG	LEU	C	59	37.519	20.223	39.377	1.00	18.52	C
ATOM	2249	CD1	LEU	C	59	36.411	21.181	39.805	1.00	14.85	C
ATOM	2250	CD2	LEU	C	59	38.147	19.538	40.574	1.00	18.90	C
ATOM	2251	N	LEU	C	60	38.399	19.348	35.553	1.00	19.17	N
ATOM	2252	CA	LEU	C	60	39.549	19.854	34.840	1.00	20.10	C
ATOM	2253	C	LEU	C	60	39.173	20.833	33.766	1.00	22.23	C
ATOM	2254	O	LEU	C	60	39.912	21.768	33.474	1.00	24.00	O
ATOM	2255	CB	LEU	C	60	40.290	18.718	34.206	1.00	18.56	C
ATOM	2256	CG	LEU	C	60	41.582	19.115	33.520	1.00	19.76	C
ATOM	2257	CD1	LEU	C	60	42.638	19.404	34.561	1.00	17.43	C
ATOM	2258	CD2	LEU	C	60	42.018	18.002	32.555	1.00	20.53	C
ATOM	2259	N	ASP	C	61	37.984	20.629	33.214	1.00	25.53	N
ATOM	2260	CA	ASP	C	61	37.471	21.478	32.157	1.00	27.32	C
ATOM	2261	C	ASP	C	61	36.950	22.809	32.666	1.00	24.92	C
ATOM	2262	O	ASP	C	61	36.768	23.738	31.883	1.00	26.04	O
ATOM	2263	CB	ASP	C	61	36.365	20.729	31.389	1.00	35.92	C
ATOM	2264	CG	ASP	C	61	36.753	19.367	30.759	1.00	45.09	C
ATOM	2265	OD1	ASP	C	61	37.808	19.241	30.086	1.00	48.21	O
ATOM	2266	OD2	ASP	C	61	35.970	18.414	30.956	1.00	49.47	O
ATOM	2267	N	LYS	C	62	36.733	22.956	33.979	1.00	22.12	N
ATOM	2268	CA	LYS	C	62	36.379	24.234	34.559	1.00	18.62	C
ATOM	2269	C	LYS	C	62	37.603	25.082	34.727	1.00	17.52	C
ATOM	2270	O	LYS	C	62	37.491	26.205	35.176	1.00	19.68	O
ATOM	2271	CB	LYS	C	62	35.718	24.064	35.888	1.00	17.21	C
ATOM	2272	CG	LYS	C	62	34.590	23.048	35.893	1.00	20.59	C
ATOM	2273	CD	LYS	C	62	33.552	23.302	34.802	1.00	23.94	C
ATOM	2274	CE	LYS	C	62	32.302	22.398	34.907	1.00	27.69	C
ATOM	2275	NZ	LYS	C	62	32.621	20.990	35.112	1.00	33.53	N
ATOM	2276	N	PHE	C	63	38.792	24.629	34.385	1.00	16.95	N
ATOM	2277	CA	PHE	C	63	39.980	25.398	34.650	1.00	18.75	C
ATOM	2278	C	PHE	C	63	40.714	25.584	33.363	1.00	20.52	C
ATOM	2279	O	PHE	C	63	40.491	24.894	32.375	1.00	22.83	O
ATOM	2280	CB	PHE	C	63	40.890	24.728	35.712	1.00	16.49	C
ATOM	2281	CG	PHE	C	63	40.280	24.790	37.109	1.00	15.86	C
ATOM	2282	CD1	PHE	C	63	40.413	25.931	37.893	1.00	15.21	C
ATOM	2283	CD2	PHE	C	63	39.475	23.764	37.555	1.00	16.14	C
ATOM	2284	CE1	PHE	C	63	39.717	26.070	39.078	1.00	11.64	C
ATOM	2285	CE2	PHE	C	63	38.742	23.932	38.732	1.00	17.01	C
ATOM	2286	CZ	PHE	C	63	38.864	25.086	39.487	1.00	11.68	C

Figure 8-49

ATOM	2287	N	SER	C	64	41.606	26.540	33.393	1.00	22.26	N
ATOM	2288	CA	SER	C	64	42.458	26.748	32.268	1.00	25.03	C
ATOM	2289	C	SER	C	64	43.928	26.724	32.651	1.00	27.32	C
ATOM	2290	O	SER	C	64	44.339	27.274	33.668	1.00	29.54	O
ATOM	2291	CB	SER	C	64	41.951	28.036	31.682	1.00	27.42	C
ATOM	2292	OG	SER	C	64	42.936	28.782	30.987	1.00	33.90	O
ATOM	2293	N	ASN	C	65	44.750	26.056	31.838	1.00	29.09	N
ATOM	2294	CA	ASN	C	65	46.183	25.967	32.048	1.00	29.94	C
ATOM	2295	C	ASN	C	65	46.912	27.280	31.894	1.00	31.16	C
ATOM	2296	O	ASN	C	65	46.482	28.228	31.252	1.00	32.15	O
ATOM	2297	CB	ASN	C	65	46.770	24.950	31.088	1.00	31.52	C
ATOM	2298	CG	ASN	C	65	48.076	24.325	31.558	1.00	31.71	C
ATOM	2299	OD1	ASN	C	65	48.626	24.591	32.636	1.00	30.12	O
ATOM	2300	ND2	ASN	C	65	48.554	23.457	30.676	1.00	32.43	N
ATOM	2301	N	ILE	C	66	48.053	27.328	32.558	1.00	34.70	N
ATOM	2302	CA	ILE	C	66	48.822	28.549	32.743	1.00	38.02	C
ATOM	2303	C	ILE	C	66	50.279	28.139	32.567	1.00	39.89	C
ATOM	2304	O	ILE	C	66	50.733	27.095	33.077	1.00	40.56	O
ATOM	2305	CB	ILE	C	66	48.560	29.130	34.181	1.00	37.96	C
ATOM	2306	CG1	ILE	C	66	47.097	29.513	34.381	1.00	37.79	C
ATOM	2307	CG2	ILE	C	66	49.443	30.334	34.443	1.00	37.53	C
ATOM	2308	CD1	ILE	C	66	46.677	29.759	35.833	1.00	39.98	C
ATOM	2309	N	SER	C	67	50.960	29.038	31.828	1.00	41.75	N
ATOM	2310	CA	SER	C	67	52.349	28.856	31.397	1.00	44.33	C
ATOM	2311	C	SER	C	67	53.320	28.647	32.536	1.00	44.00	C
ATOM	2312	O	SER	C	67	54.160	27.762	32.527	1.00	44.13	O
ATOM	2313	CB	SER	C	67	52.833	30.063	30.588	1.00	45.04	C
ATOM	2314	OG	SER	C	67	52.984	31.250	31.372	1.00	50.12	O
ATOM	2315	N	GLU	C	68	53.150	29.510	33.517	1.00	46.29	N
ATOM	2316	CA	GLU	C	68	53.969	29.520	34.702	1.00	49.75	C
ATOM	2317	C	GLU	C	68	53.215	29.731	36.043	1.00	48.90	C
ATOM	2318	O	GLU	C	68	52.374	30.624	36.267	1.00	49.09	O
ATOM	2319	CB	GLU	C	68	55.066	30.581	34.479	1.00	53.81	C
ATOM	2320	CG	GLU	C	68	56.220	30.174	33.547	1.00	59.46	C
ATOM	2321	CD	GLU	C	68	57.364	29.378	34.192	1.00	63.46	C
ATOM	2322	OE1	GLU	C	68	57.165	28.736	35.239	1.00	65.40	O
ATOM	2323	OE2	GLU	C	68	58.477	29.413	33.642	1.00	65.78	O
ATOM	2324	N	GLY	C	69	53.643	28.896	36.995	1.00	46.18	N
ATOM	2325	CA	GLY	C	69	52.938	28.734	38.244	1.00	41.09	C
ATOM	2326	C	GLY	C	69	52.252	27.398	38.142	1.00	37.69	C
ATOM	2327	O	GLY	C	69	51.845	26.975	37.057	1.00	38.22	O
ATOM	2328	N	LEU	C	70	52.181	26.712	39.279	1.00	34.58	N
ATOM	2329	CA	LEU	C	70	51.394	25.484	39.399	1.00	30.54	C
ATOM	2330	C	LEU	C	70	49.895	25.821	39.513	1.00	28.30	C
ATOM	2331	O	LEU	C	70	49.411	26.367	40.513	1.00	29.19	O
ATOM	2332	CB	LEU	C	70	51.895	24.714	40.615	1.00	28.69	C
ATOM	2333	CG	LEU	C	70	51.380	23.328	40.950	1.00	27.08	C
ATOM	2334	CD1	LEU	C	70	51.749	22.340	39.816	1.00	26.63	C
ATOM	2335	CD2	LEU	C	70	51.914	22.939	42.329	1.00	22.67	C
ATOM	2336	N	SER	C	71	49.173	25.536	38.430	1.00	23.37	N
ATOM	2337	CA	SER	C	71	47.795	25.909	38.342	1.00	18.79	C
ATOM	2338	C	SER	C	71	46.961	24.732	38.737	1.00	14.59	C
ATOM	2339	O	SER	C	71	47.420	23.616	38.830	1.00	13.92	O
ATOM	2340	CB	SER	C	71	47.499	26.362	36.929	1.00	19.04	C
ATOM	2341	OG	SER	C	71	47.794	25.282	36.073	1.00	21.34	O
ATOM	2342	N	ASN	C	72	45.691	25.004	38.938	1.00	15.21	N
ATOM	2343	CA	ASN	C	72	44.712	24.002	39.262	1.00	16.38	C
ATOM	2344	C	ASN	C	72	44.530	23.023	38.120	1.00	17.89	C
ATOM	2345	O	ASN	C	72	44.330	21.836	38.358	1.00	19.68	O
ATOM	2346	CB	ASN	C	72	43.395	24.668	39.627	1.00	14.20	C

Figure 8-50

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ATOM   2347  CG  ASN C  72      43.443  25.398  40.958  1.00 16.98           C
ATOM   2348  OD1 ASN C  72      44.439  25.399  41.698  1.00 15.50           O
ATOM   2349  ND2 ASN C  72      42.348  26.051  41.315  1.00 16.58           N
ATOM   2350  N   TYR C  73      44.626  23.493  36.878  1.00 17.45           N
ATOM   2351  CA  TYR C  73      44.546  22.649  35.715  1.00 16.35           C
ATOM   2352  C   TYR C  73      45.628  21.603  35.846  1.00 16.88           C
ATOM   2353  O   TYR C  73      45.388  20.407  35.803  1.00 18.90           O
ATOM   2354  CB  TYR C  73      44.797  23.540  34.503  1.00 14.79           C
ATOM   2355  CG  TYR C  73      44.618  22.779  33.215  1.00 18.01           C
ATOM   2356  CD1 TYR C  73      45.649  22.000  32.745  1.00 18.75           C
ATOM   2357  CD2 TYR C  73      43.428  22.809  32.544  1.00 17.80           C
ATOM   2358  CE1 TYR C  73      45.507  21.189  31.632  1.00 23.12           C
ATOM   2359  CE2 TYR C  73      43.282  22.000  31.424  1.00 23.77           C
ATOM   2360  CZ  TYR C  73      44.300  21.160  30.987  1.00 22.85           C
ATOM   2361  OH  TYR C  73      44.105  20.242  29.959  1.00 27.47           O
ATOM   2362  N   SER C  74      46.846  22.071  36.054  1.00 19.27           N
ATOM   2363  CA  SER C  74      48.037  21.234  36.196  1.00 18.80           C
ATOM   2364  C   SER C  74      47.939  20.205  37.316  1.00 18.49           C
ATOM   2365  O   SER C  74      48.192  19.026  37.062  1.00 18.14           O
ATOM   2366  CB  SER C  74      49.160  22.197  36.410  1.00 19.97           C
ATOM   2367  OG  SER C  74      50.345  21.552  36.749  1.00 27.05           O
ATOM   2368  N   ILE C  75      47.536  20.603  38.532  1.00 17.15           N
ATOM   2369  CA  ILE C  75      47.360  19.670  39.640  1.00 15.78           C
ATOM   2370  C   ILE C. 75      46.266  18.688  39.303  1.00 15.56           C
ATOM   2371  O   ILE C  75      46.392  17.487  39.540  1.00 15.90           O
ATOM   2372  CB  ILE C  75      47.004  20.373  40.994  1.00 14.47           C
ATOM   2373  CG1 ILE C  75      48.069  21.396  41.311  1.00 15.08           C
ATOM   2374  CG2 ILE C  75      46.847  19.406  42.151  1.00  9.44           C
ATOM   2375  CD1 ILE C  75      47.662  22.494  42.334  1.00 16.06           C
ATOM   2376  N   ILE C  76      45.174  19.165  38.739  1.00 15.87           N
ATOM   2377  CA  ILE C  76      44.072  18.254  38.540  1.00 16.45           C
ATOM   2378  C   ILE C  76      44.423  17.278  37.416  1.00 18.42           C
ATOM   2379  O   ILE C  76      44.047  16.107  37.479  1.00 21.96           O
ATOM   2380  CB  ILE C  76      42.777  19.029  38.276  1.00 16.99           C
ATOM   2381  CG1 ILE C  76      42.407  20.014  39.366  1.00 18.36           C
ATOM   2382  CG2 ILE C  76      41.661  18.026  38.294  1.00 18.72           C
ATOM   2383  CD1 ILE C  76      41.376  21.090  38.981  1.00 13.71           C
ATOM   2384  N   ASP C  77      45.169  17.686  36.395  1.00 19.28           N
ATOM   2385  CA  ASP C  77      45.673  16.806  35.340  1.00 20.35           C
ATOM   2386  C   ASP C  77      46.477  15.616  35.867  1.00 18.75           C
ATOM   2387  O   ASP C  77      46.259  14.474  35.483  1.00 20.55           O
ATOM   2388  CB  ASP C  77      46.528  17.679  34.388  1.00 23.72           C
ATOM   2389  CG  ASP C  77      46.796  17.143  32.984  1.00 27.17           C
ATOM   2390  OD1 ASP C  77      46.195  16.148  32.611  1.00 29.11           O
ATOM   2391  OD2 ASP C  77      47.586  17.723  32.239  1.00 31.91           O
ATOM   2392  N   LYS C  78      47.401  15.826  36.791  1.00 18.00           N
ATOM   2393  CA  LYS C  78      48.064  14.729  37.494  1.00 19.18           C
ATOM   2394  C   LYS C  78      47.114  13.802  38.229  1.00 16.84           C
ATOM   2395  O   LYS C  78      47.200  12.586  38.170  1.00 18.34           O
ATOM   2396  CB  LYS C  78      49.017  15.288  38.533  1.00 21.80           C
ATOM   2397  CG  LYS C  78      50.492  15.453  38.249  1.00 26.26           C
ATOM   2398  CD  LYS C  78      50.799  16.212  36.977  1.00 33.33           C
ATOM   2399  CE  LYS C  78      51.977  17.190  37.154  1.00 36.36           C
ATOM   2400  NZ  LYS C  78      51.538  18.516  37.592  1.00 40.57           N
ATOM   2401  N   LEU C  79      46.160  14.358  38.937  1.00 17.71           N
ATOM   2402  CA  LEU C  79      45.282  13.528  39.739  1.00 19.39           C
ATOM   2403  C   LEU C  79      44.465  12.641  38.836  1.00 19.34           C
ATOM   2404  O   LEU C  79      44.358  11.479  39.161  1.00 22.92           O
ATOM   2405  CB  LEU C  79      44.412  14.342  40.708  1.00 15.20           C
ATOM   2406  CG  LEU C  79      45.179  15.238  41.695  1.00 14.54           C
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Figure 8-51

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ATOM   2407  CD1 LEU C  79      44.276  15.934  42.683  1.00 15.95           C
ATOM   2408  CD2 LEU C  79      46.119  14.401  42.497  1.00 14.50           C
ATOM   2409  N   VAL C  80      43.974  13.115  37.694  1.00 20.79           N
ATOM   2410  CA  VAL C  80      43.210  12.349  36.719  1.00 19.75           C
ATOM   2411  C   VAL C  80      44.068  11.231  36.229  1.00 20.92           C
ATOM   2412  O   VAL C  80      43.583  10.133  36.160  1.00 19.45           O
ATOM   2413  CB  VAL C  80      42.850  13.201  35.502  1.00 20.41           C
ATOM   2414  CG1 VAL C  80      42.103  12.364  34.477  1.00 22.80           C
ATOM   2415  CG2 VAL C  80      41.915  14.311  35.902  1.00 19.35           C
ATOM   2416  N   ASN C  81      45.344  11.472  35.936  1.00 24.00           N
ATOM   2417  CA  ASN C  81      46.215  10.435  35.447  1.00 24.32           C
ATOM   2418  C   ASN C  81      46.460   9.366  36.474  1.00 25.83           C
ATOM   2419  O   ASN C  81      46.405   8.188  36.168  1.00 27.41           O
ATOM   2420  CB  ASN C  81      47.505  11.049  35.027  1.00 25.29           C
ATOM   2421  CG  ASN C  81      47.389  11.689  33.658  1.00 27.98           C
ATOM   2422  OD1 ASN C  81      47.347  10.977  32.667  1.00 30.37           O
ATOM   2423  ND2 ASN C  81      47.387  13.000  33.477  1.00 27.47           N
ATOM   2424  N   ILE C  82      46.690   9.750  37.714  1.00 27.31           N
ATOM   2425  CA  ILE C  82      46.839   8.819  38.814  1.00 27.48           C
ATOM   2426  C   ILE C  82      45.586   7.971  39.042  1.00 29.22           C
ATOM   2427  O   ILE C  82      45.705   6.766  39.266  1.00 32.26           O
ATOM   2428  CB  ILE C  82      47.228   9.685  40.022  1.00 26.77           C
ATOM   2429  CG1 ILE C  82      48.662  10.131  39.852  1.00 24.85           C
ATOM   2430  CG2 ILE C  82      47.046   8.977  41.344  1.00 26.49           C
ATOM   2431  CD1 ILE C  82      49.159  11.193  40.833  1.00 24.34           C
ATOM   2432  N   VAL C  83      44.371   8.547  38.968  1.00 30.80           N
ATOM   2433  CA  VAL C  83      43.099   7.834  39.209  1.00 29.90           C
ATOM   2434  C   VAL C  83      42.793   6.906  38.019  1.00 30.67           C
ATOM   2435  O   VAL C  83      42.229   5.824  38.195  1.00 29.90           O
ATOM   2436  CB  VAL C  83      41.888   8.816  39.455  1.00 27.23           C
ATOM   2437  CG1 VAL C  83      40.651   8.141  39.973  1.00 28.89           C
ATOM   2438  CG2 VAL C  83      42.154   9.759  40.558  1.00 28.33           C
ATOM   2439  N   ASP C  84      43.174   7.298  36.797  1.00 31.05           N
ATOM   2440  CA  ASP C  84      42.971   6.473  35.629  1.00 31.24           C
ATOM   2441  C   ASP C  84      43.761   5.196  35.686  1.00 32.41           C
ATOM   2442  O   ASP C  84      43.233   4.156  35.291  1.00 32.47           O
ATOM   2443  CB  ASP C  84      43.296   7.192  34.350  1.00 31.90           C
ATOM   2444  CG  ASP C  84      42.233   8.181  33.899  1.00 36.65           C
ATOM   2445  OD1 ASP C  84      41.105   8.177  34.417  1.00 37.73           O
ATOM   2446  OD2 ASP C  84      42.537   8.969  33.000  1.00 40.83           O
ATOM   2447  N   ASP C  85      44.988   5.287  36.202  1.00 31.95           N
ATOM   2448  CA  ASP C  85      45.770   4.128  36.589  1.00 34.69           C
ATOM   2449  C   ASP C  85      45.189   3.114  37.564  1.00 34.70           C
ATOM   2450  O   ASP C  85      45.464   1.921  37.471  1.00 34.86           O
ATOM   2451  CB  ASP C  85      47.030   4.593  37.248  1.00 37.43           C
ATOM   2452  CG  ASP C  85      48.101   5.028  36.290  1.00 41.26           C
ATOM   2453  OD1 ASP C  85      47.860   4.978  35.077  1.00 45.93           O
ATOM   2454  OD2 ASP C  85      49.169   5.423  36.776  1.00 43.39           O
ATOM   2455  N   LEU C  86      44.445   3.587  38.552  1.00 34.35           N
ATOM   2456  CA  LEU C  86      43.783   2.717  39.498  1.00 34.80           C
ATOM   2457  C   LEU C  86      42.525   2.164  38.889  1.00 34.98           C
ATOM   2458  O   LEU C  86      42.117   1.094  39.288  1.00 36.02           O
ATOM   2459  CB  LEU C  86      43.443   3.508  40.735  1.00 35.24           C
ATOM   2460  CG  LEU C  86      44.591   4.321  41.331  1.00 37.43           C
ATOM   2461  CD1 LEU C  86      44.052   5.240  42.407  1.00 38.91           C
ATOM   2462  CD2 LEU C  86      45.728   3.422  41.825  1.00 37.75           C
ATOM   2463  N   VAL C  87      41.886   2.866  37.939  1.00 37.37           N
ATOM   2464  CA  VAL C  87      40.748   2.365  37.175  1.00 38.56           C
ATOM   2465  C   VAL C  87      41.236   1.205  36.320  1.00 41.43           C
ATOM   2466  O   VAL C  87      40.621   0.154  36.337  1.00 43.44           O
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Figure 8-52

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ATOM   2467  CB  VAL C  87      40.167   3.478  36.302  1.00 36.61           C
ATOM   2468  CG1 VAL C  87      39.054   2.945  35.450  1.00 37.46           C
ATOM   2469  CG2 VAL C  87      39.592   4.584  37.139  1.00 35.39           C
ATOM   2470  N   GLU C  88      42.356   1.329  35.613  1.00 45.33           N
ATOM   2471  CA  GLU C  88      42.933   0.237  34.842  1.00 50.04           C
ATOM   2472  C   GLU C  88      43.480  -0.856  35.761  1.00 52.28           C
ATOM   2473  O   GLU C  88      43.503  -2.015  35.374  1.00 53.46           O
ATOM   2474  CB  GLU C  88      44.048   0.728  33.869  1.00 52.22           C
ATOM   2475  CG  GLU C  88      43.776   1.785  32.749  1.00 56.99           C
ATOM   2476  CD  GLU C  88      42.784   1.451  31.610  1.00 62.14           C
ATOM   2477  OE1 GLU C  88      42.853   0.348  31.046  1.00 66.19           O
ATOM   2478  OE2 GLU C  88      41.926   2.286  31.266  1.00 62.89           O
ATOM   2479  N   CYS C  89      43.930  -0.535  36.982  1.00 55.77           N
ATOM   2480  CA  CYS C  89      44.471  -1.508  37.936  1.00 58.72           C
ATOM   2481  C   CYS C  89      43.372  -2.333  38.578  1.00 60.22           C
ATOM   2482  O   CYS C  89      43.624  -3.464  39.000  1.00 61.13           O
ATOM   2483  CB  CYS C  89      45.285  -0.819  39.048  1.00 59.69           C
ATOM   2484  SG  CYS C  89      46.103  -1.924  40.239  1.00 65.48           S
ATOM   2485  N   VAL C  90      42.159  -1.749  38.657  1.00 61.71           N
ATOM   2486  CA  VAL C  90      40.963  -2.396  39.210  1.00 62.70           C
ATOM   2487  C   VAL C  90      40.453  -3.516  38.278  1.00 64.64           C
ATOM   2488  O   VAL C  90      40.010  -4.562  38.779  1.00 65.07           O
ATOM   2489  CB  VAL C  90      39.934  -1.260  39.622  1.00 60.49           C
ATOM   2490  CG1 VAL C  90      38.477  -1.428  39.231  1.00 58.30           C
ATOM   2491  CG2 VAL C  90      40.023  -1.060  41.125  1.00 58.40           C
ATOM   2492  N   LYS C  91      40.591  -3.348  36.938  1.00 66.41           N
ATOM   2493  CA  LYS C  91      40.281  -4.402  35.971  1.00 68.79           C
ATOM   2494  C   LYS C  91      41.219  -5.638  36.092  1.00 70.22           C
ATOM   2495  O   LYS C  91      40.715  -6.728  36.404  1.00 72.46           O
ATOM   2496  CB  LYS C  91      40.233  -3.836  34.530  1.00 68.55           C
ATOM   2497  CG  LYS C  91      39.560  -4.821  33.535  1.00 71.09           C
ATOM   2498  CD  LYS C  91      39.779  -4.534  32.028  1.00 71.78           C
ATOM   2499  CE  LYS C  91      39.128  -3.245  31.514  1.00 70.74           C
ATOM   2500  NZ  LYS C  91      39.730  -2.834  30.259  1.00 70.64           N
ATOM   2501  N   SER C 104      25.399   2.470  38.962  1.00 56.13           N
ATOM   2502  CA  SER C 104      25.444   3.921  38.739  1.00 55.65           C
ATOM   2503  C   SER C 104      24.850   4.688  39.939  1.00 52.95           C
ATOM   2504  O   SER C 104      23.647   4.968  39.947  1.00 53.89           O
ATOM   2505  CB  SER C 104      24.797   4.326  37.337  1.00 57.16           C
ATOM   2506  OG  SER C 104      23.517   3.792  36.940  1.00 56.67           O
ATOM   2507  N   PRO C 105      25.618   5.024  41.000  1.00 49.29           N
ATOM   2508  CA  PRO C 105      25.119   5.676  42.224  1.00 46.42           C
ATOM   2509  C   PRO C 105      24.631   7.146  42.171  1.00 44.43           C
ATOM   2510  O   PRO C 105      24.768   7.791  41.134  1.00 42.75           O
ATOM   2511  CB  PRO C 105      26.265   5.445  43.181  1.00 45.66           C
ATOM   2512  CG  PRO C 105      27.467   5.523  42.277  1.00 46.43           C
ATOM   2513  CD  PRO C 105      27.036   4.706  41.089  1.00 47.56           C
ATOM   2514  N   GLU C 106      24.023   7.707  43.240  1.00 44.38           N
ATOM   2515  CA  GLU C 106      23.436   9.055  43.238  1.00 43.85           C
ATOM   2516  C   GLU C 106      24.414  10.202  43.420  1.00 42.61           C
ATOM   2517  O   GLU C 106      25.293  10.113  44.289  1.00 42.69           O
ATOM   2518  CB  GLU C 106      22.321   9.281  44.289  1.00 45.50           C
ATOM   2519  CG  GLU C 106      20.936   8.664  44.035  1.00 46.22           C
ATOM   2520  CD  GLU C 106      20.404   8.761  42.607  1.00 45.82           C
ATOM   2521  OE1 GLU C 106      20.257   9.861  42.067  1.00 41.34           O
ATOM   2522  OE2 GLU C 106      20.152   7.699  42.032  1.00 48.83           O
ATOM   2523  N   PRO C 107      24.254  11.291  42.632  1.00 41.36           N
ATOM   2524  CA  PRO C 107      25.096  12.486  42.637  1.00 39.50           C
ATOM   2525  C   PRO C 107      24.873  13.318  43.850  1.00 38.28           C
ATOM   2526  O   PRO C 107      23.767  13.685  44.226  1.00 39.34           O
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Figure 8-53

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ATOM   2527  CB  PRO C 107      24.680  13.288  41.434  1.00 40.28           C
ATOM   2528  CG  PRO C 107      24.151  12.214  40.519  1.00 42.95           C
ATOM   2529  CD  PRO C 107      23.353  11.358  41.490  1.00 41.93           C
ATOM   2530  N   ARG C 108      26.012  13.570  44.436  1.00 35.97           N
ATOM   2531  CA  ARG C 108      26.055  14.439  45.561  1.00 35.65           C
ATOM   2532  C   ARG C 108      26.953  15.609  45.219  1.00 34.88           C
ATOM   2533  O   ARG C 108      27.707  15.585  44.244  1.00 35.60           O
ATOM   2534  CB  ARG C 108      26.617  13.701  46.756  1.00 39.40           C
ATOM   2535  CG  ARG C 108      25.710  12.742  47.530  1.00 44.75           C
ATOM   2536  CD  ARG C 108      25.959  12.906  49.053  1.00 48.86           C
ATOM   2537  NE  ARG C 108      25.401  11.801  49.824  1.00 52.47           N
ATOM   2538  CZ  ARG C 108      25.920  11.400  50.988  1.00 54.55           C
ATOM   2539  NH1 ARG C 108      26.919  12.095  51.582  1.00 55.13           N
ATOM   2540  NH2 ARG C 108      25.427  10.267  51.532  1.00 54.84           N
ATOM   2541  N   LEU C 109      26.850  16.651  46.046  1.00 32.80           N
ATOM   2542  CA  LEU C 109      27.686  17.851  45.949  1.00 31.31           C
ATOM   2543  C   LEU C 109      28.544  17.984  47.198  1.00 27.53           C
ATOM   2544  O   LEU C 109      28.058  17.849  48.335  1.00 29.28           O
ATOM   2545  CB  LEU C 109      26.876  19.173  45.813  1.00 30.72           C
ATOM   2546  CG  LEU C 109      25.837  19.411  44.752  1.00 29.60           C
ATOM   2547  CD1 LEU C 109      25.143  20.697  45.150  1.00 31.86           C
ATOM   2548  CD2 LEU C 109      26.433  19.432  43.347  1.00 30.24           C
ATOM   2549  N   PHE C 110      29.841  18.247  46.995  1.00 24.61           N
ATOM   2550  CA  PHE C 110      30.784  18.289  48.116  1.00 20.67           C
ATOM   2551  C   PHE C 110      31.579  19.548  48.013  1.00 17.66           C
ATOM   2552  O   PHE C 110      31.746  20.049  46.924  1.00 19.14           O
ATOM   2553  CB  PHE C 110      31.721  17.098  48.021  1.00 23.08           C
ATOM   2554  CG  PHE C 110      31.049  15.733  48.163  1.00 22.91           C
ATOM   2555  CD1 PHE C 110      30.793  15.226  49.426  1.00 20.89           C
ATOM   2556  CD2 PHE C 110      30.737  15.008  47.024  1.00 23.49           C
ATOM   2557  CE1 PHE C 110      30.269  13.969  49.565  1.00 21.28           C
ATOM   2558  CE2 PHE C 110      30.186  13.751  47.178  1.00 24.67           C
ATOM   2559  CZ  PHE C 110      29.974  13.233  48.444  1.00 24.36           C
ATOM   2560  N   THR C 111      32.071  20.116  49.084  1.00 17.78           N
ATOM   2561  CA  THR C 111      32.961  21.249  48.978  1.00 18.25           C
ATOM   2562  C   THR C 111      34.337  20.763  48.509  1.00 21.30           C
ATOM   2563  O   THR C 111      34.518  19.547  48.617  1.00 26.22           O
ATOM   2564  CB  THR C 111      33.057  21.895  50.359  1.00 19.78           C
ATOM   2565  OG1 THR C 111      33.780  20.989  51.199  1.00 19.58           O
ATOM   2566  CG2 THR C 111      31.663  22.215  50.913  1.00 18.93           C
ATOM   2567  N   PRO C 112      35.360  21.512  48.024  1.00 19.29           N
ATOM   2568  CA  PRO C 112      36.675  20.962  47.729  1.00 18.39           C
ATOM   2569  C   PRO C 112      37.225  20.086  48.855  1.00 21.30           C
ATOM   2570  O   PRO C 112      37.605  18.953  48.611  1.00 22.05           O
ATOM   2571  CB  PRO C 112      37.455  22.226  47.520  1.00 18.00           C
ATOM   2572  CG  PRO C 112      36.455  23.100  46.801  1.00 16.59           C
ATOM   2573  CD  PRO C 112      35.265  22.919  47.660  1.00 14.34           C
ATOM   2574  N   GLU C 113      37.221  20.521  50.119  1.00 22.83           N
ATOM   2575  CA  GLU C 113      37.717  19.735  51.235  1.00 24.32           C
ATOM   2576  C   GLU C 113      37.046  18.394  51.408  1.00 23.52           C
ATOM   2577  O   GLU C 113      37.729  17.385  51.549  1.00 23.92           O
ATOM   2578  CB  GLU C 113      37.496  20.463  52.524  1.00 27.24           C
ATOM   2579  CG  GLU C 113      38.700  20.955  53.281  1.00 35.37           C
ATOM   2580  CD  GLU C 113      38.282  21.200  54.724  1.00 39.80           C
ATOM   2581  OE1 GLU C 113      37.915  20.230  55.387  1.00 41.11           O
ATOM   2582  OE2 GLU C 113      38.296  22.339  55.182  1.00 41.53           O
ATOM   2583  N   GLU C 114      35.712  18.350  51.386  1.00 23.35           N
ATOM   2584  CA  GLU C 114      34.968  17.107  51.535  1.00 23.29           C
ATOM   2585  C   GLU C 114      35.168  16.200  50.344  1.00 22.72           C
ATOM   2586  O   GLU C 114      35.160  14.981  50.518  1.00 23.79           O
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Figure 8-54

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ATOM   2587  CB  GLU C 114      33.470  17.344  51.622  1.00 26.84           C
ATOM   2588  CG  GLU C 114      32.974  18.114  52.849  1.00 31.67           C
ATOM   2589  CD  GLU C 114      31.578  18.736  52.701  1.00 37.47           C
ATOM   2590  OE1 GLU C 114      30.884  18.533  51.681  1.00 35.31           O
ATOM   2591  OE2 GLU C 114      31.202  19.468  53.633  1.00 40.13           O
ATOM   2592  N   PHE C 115      35.320  16.775  49.143  1.00 20.03           N
ATOM   2593  CA  PHE C 115      35.606  15.979  47.971  1.00 18.15           C
ATOM   2594  C   PHE C 115      36.997  15.397  48.157  1.00 17.33           C
ATOM   2595  O   PHE C 115      37.214  14.205  48.013  1.00 18.05           O
ATOM   2596  CB  PHE C 115      35.524  16.833  46.705  1.00 15.90           C
ATOM   2597  CG  PHE C 115      35.825  16.063  45.429  1.00 17.09           C
ATOM   2598  CD1 PHE C 115      34.861  15.299  44.845  1.00 16.21           C
ATOM   2599  CD2 PHE C 115      37.094  16.093  44.890  1.00 18.64           C
ATOM   2600  CE1 PHE C 115      35.193  14.558  43.744  1.00 19.14           C
ATOM   2601  CE2 PHE C 115      37.425  15.336  43.795  1.00 18.76           C
ATOM   2602  CZ  PHE C 115      36.463  14.570  43.217  1.00 19.41           C
ATOM   2603  N   PHE C 116      38.010  16.167  48.509  1.00 19.36           N
ATOM   2604  CA  PHE C 116      39.361  15.618  48.454  1.00 17.90           C
ATOM   2605  C   PHE C 116      39.621  14.678  49.623  1.00 18.24           C
ATOM   2606  O   PHE C 116      40.505  13.855  49.549  1.00 19.98           O
ATOM   2607  CB  PHE C 116      40.376  16.744  48.162  1.00 16.33           C
ATOM   2608  CG  PHE C 116      40.442  17.170  46.679  1.00 15.27           C
ATOM   2609  CD1 PHE C 116      41.052  16.328  45.753  1.00 14.80           C
ATOM   2610  CD2 PHE C 116      39.806  18.324  46.240  1.00 12.85           C
ATOM   2611  CE1 PHE C 116      40.967  16.602  44.409  1.00 12.34           C
ATOM   2612  CE2 PHE C 116      39.715  18.569  44.885  1.00 14.12           C
ATOM   2613  CZ  PHE C 116      40.289  17.711  43.980  1.00 10.60           C
ATOM   2614  N   ARG C 117      38.755  14.664  50.641  1.00 20.78           N
ATOM   2615  CA  ARG C 117      38.796  13.751  51.770  1.00 21.33           C
ATOM   2616  C   ARG C 117      38.412  12.368  51.308  1.00 20.46           C
ATOM   2617  O   ARG C 117      39.076  11.405  51.639  1.00 21.70           O
ATOM   2618  CB  ARG C 117      37.823  14.244  52.840  1.00 21.70           C
ATOM   2619  CG  ARG C 117      37.838  13.513  54.177  1.00 27.63           C
ATOM   2620  CD  ARG C 117      36.826  14.115  55.165  1.00 29.36           C
ATOM   2621  NE  ARG C 117      37.230  15.464  55.616  1.00 32.11           N
ATOM   2622  CZ  ARG C 117      36.411  16.535  55.565  1.00 32.37           C
ATOM   2623  NH1 ARG C 117      35.179  16.464  55.047  1.00 32.61           N
ATOM   2624  NH2 ARG C 117      36.836  17.701  56.025  1.00 30.98           N
ATOM   2625  N   ILE C 118      37.342  12.263  50.540  1.00 21.91           N
ATOM   2626  CA  ILE C 118      36.897  11.031  49.882  1.00 22.55           C
ATOM   2627  C   ILE C 118      37.944  10.504  48.890  1.00 23.60           C
ATOM   2628  O   ILE C 118      38.254   9.316  48.853  1.00 24.72           O
ATOM   2629  CB  ILE C 118      35.527  11.358  49.213  1.00 22.47           C
ATOM   2630  CG1 ILE C 118      34.467  11.506  50.293  1.00 21.67           C
ATOM   2631  CG2 ILE C 118      35.117  10.338  48.161  1.00 21.48           C
ATOM   2632  CD1 ILE C 118      33.164  12.169  49.825  1.00 21.12           C
ATOM   2633  N   PHE C 119      38.544  11.402  48.103  1.00 23.86           N
ATOM   2634  CA  PHE C 119      39.633  11.098  47.186  1.00 22.73           C
ATOM   2635  C   PHE C 119      40.816  10.488  47.916  1.00 24.24           C
ATOM   2636  O   PHE C 119      41.233   9.416  47.511  1.00 24.28           O
ATOM   2637  CB  PHE C 119      40.038  12.357  46.426  1.00 15.88           C
ATOM   2638  CG  PHE C 119      41.297  12.224  45.624  1.00 15.30           C
ATOM   2639  CD1 PHE C 119      41.231  11.724  44.354  1.00 15.03           C
ATOM   2640  CD2 PHE C 119      42.495  12.639  46.172  1.00 12.85           C
ATOM   2641  CE1 PHE C 119      42.412  11.623  43.653  1.00 15.97           C
ATOM   2642  CE2 PHE C 119      43.675  12.526  45.473  1.00 15.16           C
ATOM   2643  CZ  PHE C 119      43.630  12.003  44.206  1.00 16.33           C
ATOM   2644  N   ASN C 120      41.396  11.145  48.936  1.00 26.61           N
ATOM   2645  CA  ASN C 120      42.511  10.621  49.728  1.00 27.10           C
ATOM   2646  C   ASN C 120      42.225   9.301  50.400  1.00 28.31           C
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Figure 8-55

ATOM	2647	O	ASN	C	120	43.081	8.433	50.376	1.00	28.63	O
ATOM	2648	CB	ASN	C	120	42.959	11.590	50.783	1.00	24.50	C
ATOM	2649	CG	ASN	C	120	43.837	12.659	50.215	1.00	27.34	C
ATOM	2650	OD1	ASN	C	120	43.864	13.757	50.761	1.00	32.26	O
ATOM	2651	ND2	ASN	C	120	44.628	12.420	49.169	1.00	29.64	N
ATOM	2652	N	ARG	C	121	41.017	9.136	50.947	1.00	30.80	N
ATOM	2653	CA	ARG	C	121	40.549	7.862	51.441	1.00	35.49	C
ATOM	2654	C	ARG	C	121	40.514	6.767	50.357	1.00	36.43	C
ATOM	2655	O	ARG	C	121	40.859	5.616	50.628	1.00	38.58	O
ATOM	2656	CB	ARG	C	121	39.202	8.108	52.138	1.00	37.63	C
ATOM	2657	CG	ARG	C	121	38.534	6.865	52.651	1.00	42.24	C
ATOM	2658	CD	ARG	C	121	37.240	7.194	53.373	1.00	47.82	C
ATOM	2659	NE	ARG	C	121	36.399	6.001	53.529	1.00	51.79	N
ATOM	2660	CZ	ARG	C	121	36.788	4.912	54.233	1.00	55.38	C
ATOM	2661	NH1	ARG	C	121	38.016	4.799	54.783	1.00	57.12	N
ATOM	2662	NH2	ARG	C	121	35.928	3.904	54.446	1.00	55.34	N
ATOM	2663	N	SER	C	122	40.171	7.089	49.106	1.00	36.49	N
ATOM	2664	CA	SER	C	122	40.274	6.177	47.974	1.00	36.44	C
ATOM	2665	C	SER	C	122	41.660	5.723	47.529	1.00	37.85	C
ATOM	2666	O	SER	C	122	41.874	4.556	47.235	1.00	39.23	O
ATOM	2667	CB	SER	C	122	39.613	6.814	46.788	1.00	34.58	C
ATOM	2668	OG	SER	C	122	38.286	7.132	47.155	1.00	34.47	O
ATOM	2669	N	ILE	C	123	42.638	6.599	47.409	1.00	38.85	N
ATOM	2670	CA	ILE	C	123	43.949	6.180	46.985	1.00	43.11	C
ATOM	2671	C	ILE	C	123	44.589	5.456	48.157	1.00	46.18	C
ATOM	2672	O	ILE	C	123	45.449	4.614	47.937	1.00	47.69	O
ATOM	2673	CB	ILE	C	123	44.843	7.378	46.505	1.00	42.65	C
ATOM	2674	CG1	ILE	C	123	44.147	8.410	45.599	1.00	38.38	C
ATOM	2675	CG2	ILE	C	123	46.146	6.866	45.872	1.00	43.09	C
ATOM	2676	CD1	ILE	C	123	43.242	7.872	44.489	1.00	35.80	C
ATOM	2677	N	ASP	C	124	44.206	5.755	49.402	1.00	50.61	N
ATOM	2678	CA	ASP	C	124	44.805	5.095	50.564	1.00	54.85	C
ATOM	2679	C	ASP	C	124	44.197	3.730	50.882	1.00	54.20	C
ATOM	2680	O	ASP	C	124	44.774	2.898	51.586	1.00	54.57	O
ATOM	2681	CB	ASP	C	124	44.788	5.989	51.823	1.00	59.47	C
ATOM	2682	CG	ASP	C	124	45.794	7.151	51.915	1.00	63.36	C
ATOM	2683	OD1	ASP	C	124	45.935	7.919	50.949	1.00	63.45	O
ATOM	2684	OD2	ASP	C	124	46.414	7.295	52.988	1.00	66.94	O
ATOM	2685	N	ALA	C	125	43.039	3.460	50.281	1.00	54.57	N
ATOM	2686	CA	ALA	C	125	42.427	2.137	50.314	1.00	56.99	C
ATOM	2687	C	ALA	C	125	43.150	1.108	49.440	1.00	58.85	C
ATOM	2688	O	ALA	C	125	42.617	0.022	49.161	1.00	59.46	O
ATOM	2689	CB	ALA	C	125	40.982	2.263	49.824	1.00	56.08	C
ATOM	2690	N	PHE	C	126	44.343	1.552	48.975	1.00	60.81	N
ATOM	2691	CA	PHE	C	126	45.408	0.793	48.316	1.00	62.82	C
ATOM	2692	C	PHE	C	126	46.675	0.603	49.241	1.00	64.91	C
ATOM	2693	O	PHE	C	126	47.801	0.492	48.731	1.00	65.88	O
ATOM	2694	CB	PHE	C	126	45.715	1.476	46.898	1.00	60.15	C
ATOM	2695	CG	PHE	C	126	44.638	1.419	45.778	1.00	57.55	C
ATOM	2696	CD1	PHE	C	126	43.594	2.334	45.731	1.00	56.09	C
ATOM	2697	CD2	PHE	C	126	44.655	0.421	44.813	1.00	56.90	C
ATOM	2698	CE1	PHE	C	126	42.568	2.227	44.807	1.00	52.24	C
ATOM	2699	CE2	PHE	C	126	43.627	0.319	43.884	1.00	54.42	C
ATOM	2700	CZ	PHE	C	126	42.573	1.208	43.889	1.00	52.99	C
TER	2702		PHE	C	126						
ATOM	2703	N	ASN	D	11	47.774	44.287	38.626	1.00	52.77	N
ATOM	2704	CA	ASN	D	11	46.416	43.904	38.273	1.00	53.01	C
ATOM	2705	C	ASN	D	11	46.383	43.039	36.995	1.00	52.04	C
ATOM	2706	O	ASN	D	11	46.673	41.852	37.139	1.00	53.30	O
ATOM	2707	CB	ASN	D	11	45.488	45.136	38.154	1.00	52.37	C

Figure 8-56

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ATOM   2708  N   VAL D  12      46.135  43.551  35.763  1.00 49.81           N
ATOM   2709  CA  VAL D  12      45.936  42.823  34.490  1.00 45.10           C
ATOM   2710  C   VAL D  12      46.697  41.529  34.194  1.00 40.73           C
ATOM   2711  O   VAL D  12      46.109  40.477  33.958  1.00 39.20           O
ATOM   2712  CB  VAL D  12      46.118  43.863  33.336  1.00 46.99           C
ATOM   2713  CG1 VAL D  12      46.377  43.229  31.966  1.00 47.11           C
ATOM   2714  CG2 VAL D  12      44.888  44.784  33.225  1.00 46.26           C
ATOM   2715  N   LYS D  13      48.014  41.610  34.165  1.00 37.97           N
ATOM   2716  CA  LYS D  13      48.844  40.432  34.132  1.00 36.45           C
ATOM   2717  C   LYS D  13      48.402  39.322  35.117  1.00 36.18           C
ATOM   2718  O   LYS D  13      48.194  38.166  34.709  1.00 37.38           O
ATOM   2719  CB  LYS D  13      50.258  40.905  34.451  1.00 35.89           C
ATOM   2720  N   ASP D  14      48.190  39.643  36.410  1.00 33.96           N
ATOM   2721  CA  ASP D  14      47.703  38.684  37.372  1.00 29.22           C
ATOM   2722  C   ASP D  14      46.220  38.409  37.305  1.00 25.55           C
ATOM   2723  O   ASP D  14      45.799  37.316  37.647  1.00 25.36           O
ATOM   2724  CB  ASP D  14      48.158  39.126  38.726  1.00 33.71           C
ATOM   2725  CG  ASP D  14      49.573  38.623  39.084  1.00 41.45           C
ATOM   2726  OD1 ASP D  14      50.178  37.858  38.316  1.00 45.64           O
ATOM   2727  OD2 ASP D  14      50.083  38.981  40.161  1.00 44.73           O
ATOM   2728  N   VAL D  15      45.421  39.347  36.809  1.00 22.15           N
ATOM   2729  CA  VAL D  15      44.000  39.173  36.672  1.00 19.73           C
ATOM   2730  C   VAL D  15      43.683  38.044  35.731  1.00 21.56           C
ATOM   2731  O   VAL D  15      42.825  37.217  36.016  1.00 23.37           O
ATOM   2732  CB  VAL D  15      43.294  40.462  36.234  1.00 18.49           C
ATOM   2733  CG1 VAL D  15      41.883  40.238  35.684  1.00 17.31           C
ATOM   2734  CG2 VAL D  15      43.093  41.327  37.450  1.00 17.77           C
ATOM   2735  N   THR D  16      44.387  37.974  34.623  1.00 22.81           N
ATOM   2736  CA  THR D  16      44.166  36.943  33.605  1.00 24.47           C
ATOM   2737  C   THR D  16      44.517  35.513  34.082  1.00 21.91           C
ATOM   2738  O   THR D  16      43.904  34.526  33.676  1.00 20.78           O
ATOM   2739  CB  THR D  16      44.991  37.520  32.381  1.00 26.36           C
ATOM   2740  OG1 THR D  16      44.076  38.310  31.630  1.00 28.31           O
ATOM   2741  CG2 THR D  16      45.721  36.529  31.530  1.00 28.93           C
ATOM   2742  N   LYS D  17      45.470  35.415  35.016  1.00 20.72           N
ATOM   2743  CA  LYS D  17      45.958  34.179  35.596  1.00 20.21           C
ATOM   2744  C   LYS D  17      45.019  33.719  36.683  1.00 18.63           C
ATOM   2745  O   LYS D  17      44.754  32.526  36.783  1.00 21.04           O
ATOM   2746  CB  LYS D  17      47.277  34.522  36.207  1.00 24.75           C
ATOM   2747  CG  LYS D  17      48.163  33.373  36.590  1.00 29.44           C
ATOM   2748  CD  LYS D  17      49.365  33.928  37.347  1.00 32.96           C
ATOM   2749  CE  LYS D  17      50.423  34.474  36.422  1.00 36.20           C
ATOM   2750  NZ  LYS D  17      51.313  35.272  37.230  1.00 39.87           N
ATOM   2751  N   LEU D  18      44.483  34.656  37.468  1.00 16.11           N
ATOM   2752  CA  LEU D  18      43.391  34.389  38.362  1.00 13.77           C
ATOM   2753  C   LEU D  18      42.158  33.926  37.636  1.00 14.10           C
ATOM   2754  O   LEU D  18      41.662  32.898  38.072  1.00 17.61           O
ATOM   2755  CB  LEU D  18      43.070  35.599  39.180  1.00 14.87           C
ATOM   2756  CG  LEU D  18      42.103  35.485  40.362  1.00 15.58           C
ATOM   2757  CD1 LEU D  18      42.567  34.568  41.470  1.00 11.31           C
ATOM   2758  CD2 LEU D  18      41.872  36.849  40.952  1.00 15.28           C
ATOM   2759  N   VAL D  19      41.617  34.544  36.561  1.00 15.42           N
ATOM   2760  CA  VAL D  19      40.479  34.034  35.786  1.00 13.39           C
ATOM   2761  C   VAL D  19      40.704  32.587  35.385  1.00 14.30           C
ATOM   2762  O   VAL D  19      39.824  31.744  35.542  1.00 13.93           O
ATOM   2763  CB  VAL D  19      40.251  34.838  34.489  1.00 14.39           C
ATOM   2764  CG1 VAL D  19      39.059  34.330  33.694  1.00 11.41           C
ATOM   2765  CG2 VAL D  19      39.913  36.255  34.797  1.00 12.80           C
ATOM   2766  N   ALA D  20      41.911  32.288  34.876  1.00 14.50           N
ATOM   2767  CA  ALA D  20      42.319  30.924  34.543  1.00 15.90           C
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Figure 8-57

ATOM	2768	C	ALA	D	20	42.340	29.894	35.680	1.00	16.27	C
ATOM	2769	O	ALA	D	20	42.153	28.697	35.464	1.00	14.91	O
ATOM	2770	CB	ALA	D	20	43.719	30.983	33.946	1.00	16.48	C
ATOM	2771	N	ASN	D	21	42.543	30.396	36.914	1.00	16.20	N
ATOM	2772	CA	ASN	D	21	42.665	29.549	38.081	1.00	14.59	C
ATOM	2773	C	ASN	D	21	41.408	29.513	38.923	1.00	15.22	C
ATOM	2774	O	ASN	D	21	41.343	28.894	39.982	1.00	14.76	O
ATOM	2775	CB	ASN	D	21	43.863	30.085	38.853	1.00	15.31	C
ATOM	2776	CG	ASN	D	21	44.760	29.000	39.360	1.00	12.22	C
ATOM	2777	OD1	ASN	D	21	45.002	28.023	38.669	1.00	15.31	O
ATOM	2778	ND2	ASN	D	21	45.313	29.122	40.545	1.00	14.81	N
ATOM	2779	N	LEU	D	22	40.364	30.201	38.493	1.00	15.62	N
ATOM	2780	CA	LEU	D	22	39.069	30.126	39.157	1.00	15.32	C
ATOM	2781	C	LEU	D	22	38.172	29.241	38.319	1.00	15.81	C
ATOM	2782	O	LEU	D	22	38.337	29.289	37.109	1.00	18.22	O
ATOM	2783	CB	LEU	D	22	38.470	31.498	39.326	1.00	11.04	C
ATOM	2784	CG	LEU	D	22	39.203	32.454	40.210	1.00	10.12	C
ATOM	2785	CD1	LEU	D	22	38.580	33.801	40.004	1.00	11.85	C
ATOM	2786	CD2	LEU	D	22	39.108	32.071	41.671	1.00	10.74	C
ATOM	2787	N	PRO	D	23	37.246	28.422	38.825	1.00	16.11	N
ATOM	2788	CA	PRO	D	23	36.365	27.588	38.004	1.00	15.30	C
ATOM	2789	C	PRO	D	23	35.533	28.456	37.064	1.00	16.55	C
ATOM	2790	O	PRO	D	23	35.044	29.485	37.502	1.00	18.78	O
ATOM	2791	CB	PRO	D	23	35.474	26.944	39.027	1.00	14.03	C
ATOM	2792	CG	PRO	D	23	36.252	27.043	40.317	1.00	16.22	C
ATOM	2793	CD	PRO	D	23	36.854	28.409	40.228	1.00	15.04	C
ATOM	2794	N	LYS	D	24	35.319	28.105	35.785	1.00	19.22	N
ATOM	2795	CA	LYS	D	24	34.492	28.864	34.822	1.00	19.57	C
ATOM	2796	C	LYS	D	24	33.027	28.975	35.241	1.00	18.94	C
ATOM	2797	O	LYS	D	24	32.381	29.956	34.910	1.00	22.65	O
ATOM	2798	CB	LYS	D	24	34.575	28.214	33.425	1.00	20.25	C
ATOM	2799	CG	LYS	D	24	35.853	28.425	32.655	1.00	19.83	C
ATOM	2800	CD	LYS	D	24	36.049	27.261	31.683	1.00	20.33	C
ATOM	2801	CE	LYS	D	24	37.542	27.297	31.291	1.00	25.04	C
ATOM	2802	NZ	LYS	D	24	38.019	26.084	30.623	1.00	27.36	N
ATOM	2803	N	ASP	D	25	32.490	28.011	36.007	1.00	20.97	N
ATOM	2804	CA	ASP	D	25	31.146	27.984	36.585	1.00	20.24	C
ATOM	2805	C	ASP	D	25	31.084	28.420	38.037	1.00	20.26	C
ATOM	2806	O	ASP	D	25	30.092	28.177	38.714	1.00	24.64	O
ATOM	2807	CB	ASP	D	25	30.557	26.555	36.502	1.00	21.95	C
ATOM	2808	CG	ASP	D	25	31.274	25.501	37.333	1.00	26.54	C
ATOM	2809	OD1	ASP	D	25	32.429	25.721	37.693	1.00	28.24	O
ATOM	2810	OD2	ASP	D	25	30.697	24.445	37.616	1.00	29.75	O
ATOM	2811	N	TYR	D	26	32.109	29.038	38.591	1.00	19.65	N
ATOM	2812	CA	TYR	D	26	31.978	29.716	39.865	1.00	19.99	C
ATOM	2813	C	TYR	D	26	31.327	31.078	39.666	1.00	20.55	C
ATOM	2814	O	TYR	D	26	31.837	31.882	38.892	1.00	23.24	O
ATOM	2815	CB	TYR	D	26	33.388	29.886	40.446	1.00	18.93	C
ATOM	2816	CG	TYR	D	26	33.487	30.459	41.844	1.00	18.30	C
ATOM	2817	CD1	TYR	D	26	32.718	29.938	42.855	1.00	17.48	C
ATOM	2818	CD2	TYR	D	26	34.309	31.538	42.057	1.00	19.75	C
ATOM	2819	CE1	TYR	D	26	32.689	30.542	44.078	1.00	17.10	C
ATOM	2820	CE2	TYR	D	26	34.304	32.124	43.291	1.00	21.03	C
ATOM	2821	CZ	TYR	D	26	33.494	31.613	44.276	1.00	19.84	C
ATOM	2822	OH	TYR	D	26	33.553	32.163	45.538	1.00	26.79	O
HETATM	2823	N	MSE	D	27	30.240	31.351	40.390	1.00	20.11	N
HETATM	2824	CA	MSE	D	27	29.563	32.640	40.409	1.00	19.68	C
HETATM	2825	C	MSE	D	27	29.972	33.547	41.554	1.00	19.24	C
HETATM	2826	O	MSE	D	27	29.844	33.217	42.722	1.00	18.84	O
HETATM	2827	CB	MSE	D	27	28.030	32.478	40.470	1.00	25.00	C

Figure 8-58

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HETATM 2828  CG  MSE D  27      27.356  31.633  39.361  1.00 27.34           C
HETATM 2829  SE  MSE D  27      28.005  31.953  37.549  1.00 33.76          SE
HETATM 2830  CE  MSE D  27      27.146  33.538  37.334  1.00 29.16           C
ATOM   2831  N   ILE D  28      30.503  34.700  41.191  1.00 18.26           N
ATOM   2832  CA  ILE D  28      30.838  35.733  42.127  1.00 18.98           C
ATOM   2833  C   ILE D  28      29.668  36.703  42.239  1.00 19.61           C
ATOM   2834  O   ILE D  28      29.151  37.088  41.196  1.00 22.18           O
ATOM   2835  CB  ILE D  28      32.136  36.421  41.662  1.00 15.61           C
ATOM   2836  CG1 ILE D  28      33.234  35.398  41.469  1.00 12.73           C
ATOM   2837  CG2 ILE D  28      32.593  37.471  42.693  1.00 15.00           C
ATOM   2838  CD1 ILE D  28      34.487  35.969  40.818  1.00 10.07           C
ATOM   2839  N   THR D  29      29.199  37.105  43.433  1.00 20.30           N
ATOM   2840  CA  THR D  29      28.142  38.118  43.587  1.00 18.55           C
ATOM   2841  C   THR D  29      28.720  39.514  43.593  1.00 18.51           C
ATOM   2842  O   THR D  29      29.681  39.757  44.305  1.00 20.24           O
ATOM   2843  CB  THR D  29      27.248  37.915  44.853  1.00 18.42           C
ATOM   2844  OG1 THR D  29      26.791  36.570  44.817  1.00 20.41           O
ATOM   2845  CG2 THR D  29      25.982  38.747  44.836  1.00 16.39           C
ATOM   2846  N   LEU D  30      28.205  40.455  42.785  1.00 18.52           N
ATOM   2847  CA  LEU D  30      28.610  41.845  42.783  1.00 17.78           C
ATOM   2848  C   LEU D  30      27.305  42.598  42.724  1.00 19.35           C
ATOM   2849  O   LEU D  30      26.420  42.245  41.946  1.00 19.98           O
ATOM   2850  CB  LEU D  30      29.390  42.149  41.505  1.00 18.28           C
ATOM   2851  CG  LEU D  30      29.905  43.557  41.154  1.00 15.52           C
ATOM   2852  CD1 LEU D  30      30.720  44.170  42.241  1.00 15.62           C
ATOM   2853  CD2 LEU D  30      30.732  43.522  39.879  1.00 17.11           C
ATOM   2854  N   LYS D  31      27.150  43.613  43.560  1.00 20.05           N
ATOM   2855  CA  LYS D  31      26.046  44.522  43.409  1.00 21.35           C
ATOM   2856  C   LYS D  31      26.413  45.564  42.354  1.00 23.46           C
ATOM   2857  O   LYS D  31      27.223  46.470  42.561  1.00 23.96           O
ATOM   2858  CB  LYS D  31      25.702  45.148  44.722  1.00 21.22           C
ATOM   2859  CG  LYS D  31      25.353  44.109  45.766  1.00 23.53           C
ATOM   2860  CD  LYS D  31      24.738  44.814  46.976  1.00 28.13           C
ATOM   2861  CE  LYS D  31      24.583  43.890  48.182  1.00 29.07           C
ATOM   2862  NZ  LYS D  31      23.982  44.617  49.293  1.00 34.24           N
ATOM   2863  N   TYR D  32      25.818  45.356  41.172  1.00 25.01           N
ATOM   2864  CA  TYR D  32      26.219  46.004  39.925  1.00 25.06           C
ATOM   2865  C   TYR D  32      25.377  47.248  39.752  1.00 26.53           C
ATOM   2866  O   TYR D  32      24.167  47.293  40.046  1.00 27.71           O
ATOM   2867  CB  TYR D  32      26.050  44.978  38.778  1.00 25.42           C
ATOM   2868  CG  TYR D  32      26.196  45.465  37.336  1.00 24.15           C
ATOM   2869  CD1 TYR D  32      27.433  45.460  36.728  1.00 22.29           C
ATOM   2870  CD2 TYR D  32      25.071  45.915  36.672  1.00 23.90           C
ATOM   2871  CE1 TYR D  32      27.558  45.961  35.459  1.00 24.06           C
ATOM   2872  CE2 TYR D  32      25.183  46.427  35.409  1.00 25.00           C
ATOM   2873  CZ  TYR D  32      26.427  46.458  34.822  1.00 26.48           C
ATOM   2874  OH  TYR D  32      26.533  47.012  33.558  1.00 26.81           O
ATOM   2875  N   VAL D  33      26.099  48.297  39.333  1.00 28.52           N
ATOM   2876  CA  VAL D  33      25.505  49.613  39.093  1.00 27.57           C
ATOM   2877  C   VAL D  33      24.973  49.634  37.670  1.00 27.14           C
ATOM   2878  O   VAL D  33      25.769  49.693  36.750  1.00 28.15           O
ATOM   2879  CB  VAL D  33      26.529  50.724  39.288  1.00 26.82           C
ATOM   2880  CG1 VAL D  33      25.931  52.066  38.921  1.00 25.83           C
ATOM   2881  CG2 VAL D  33      26.880  50.758  40.755  1.00 25.22           C
ATOM   2882  N   PRO D  34      23.674  49.548  37.434  1.00 27.51           N
ATOM   2883  CA  PRO D  34      23.085  49.608  36.105  1.00 28.26           C
ATOM   2884  C   PRO D  34      23.491  50.909  35.413  1.00 31.20           C
ATOM   2885  O   PRO D  34      23.649  51.980  36.012  1.00 32.62           O
ATOM   2886  CB  PRO D  34      21.617  49.574  36.407  1.00 27.82           C
ATOM   2887  CG  PRO D  34      21.523  48.866  37.750  1.00 29.77           C
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Figure 8-59

ATOM	2888	CD	PRO	D	34	22.668	49.494	38.488	1.00	27.97	C
ATOM	2889	N	GLY	D	35	23.756	50.780	34.117	1.00	32.89	N
ATOM	2890	CA	GLY	D	35	24.265	51.891	33.338	1.00	34.68	C
ATOM	2891	C	GLY	D	35	25.749	52.065	33.438	1.00	34.91	C
ATOM	2892	O	GLY	D	35	26.271	53.066	32.991	1.00	38.32	O
HETATM	2893	N	MSE	D	36	26.456	51.105	33.995	1.00	36.03	N
HETATM	2894	CA	MSE	D	36	27.910	51.084	34.060	1.00	38.11	C
HETATM	2895	C	MSE	D	36	28.634	51.193	32.726	1.00	38.57	C
HETATM	2896	O	MSE	D	36	29.741	51.717	32.594	1.00	39.99	O
HETATM	2897	CB	MSE	D	36	28.255	49.744	34.622	1.00	41.60	C
HETATM	2898	CG	MSE	D	36	28.972	49.795	35.911	1.00	45.00	C
HETATM	2899	SE	MSE	D	36	30.412	48.532	35.745	1.00	54.90	SE
HETATM	2900	CE	MSE	D	36	30.966	48.492	33.897	1.00	45.21	C
ATOM	2901	N	ASP	D	37	27.956	50.571	31.760	1.00	39.01	N
ATOM	2902	CA	ASP	D	37	28.357	50.446	30.370	1.00	37.84	C
ATOM	2903	C	ASP	D	37	28.125	51.687	29.525	1.00	37.29	C
ATOM	2904	O	ASP	D	37	29.067	52.169	28.896	1.00	40.17	O
ATOM	2905	CB	ASP	D	37	27.725	49.194	29.760	1.00	37.35	C
ATOM	2906	CG	ASP	D	37	26.258	48.854	30.083	1.00	40.62	C
ATOM	2907	OD1	ASP	D	37	25.560	49.672	30.709	1.00	39.43	O
ATOM	2908	OD2	ASP	D	37	25.813	47.752	29.705	1.00	41.13	O
ATOM	2909	N	VAL	D	38	26.930	52.266	29.525	1.00	36.85	N
ATOM	2910	CA	VAL	D	38	26.665	53.462	28.719	1.00	38.43	C
ATOM	2911	C	VAL	D	38	27.021	54.828	29.311	1.00	39.02	C
ATOM	2912	O	VAL	D	38	27.395	55.748	28.581	1.00	39.83	O
ATOM	2913	CB	VAL	D	38	25.212	53.466	28.171	1.00	36.76	C
ATOM	2914	CG1	VAL	D	38	25.086	52.227	27.356	1.00	36.24	C
ATOM	2915	CG2	VAL	D	38	24.081	53.482	29.175	1.00	36.31	C
ATOM	2916	N	LEU	D	39	26.886	54.965	30.641	1.00	39.92	N
ATOM	2917	CA	LEU	D	39	27.031	56.231	31.341	1.00	38.96	C
ATOM	2918	C	LEU	D	39	28.495	56.624	31.625	1.00	41.40	C
ATOM	2919	O	LEU	D	39	29.397	55.777	31.589	1.00	40.82	O
ATOM	2920	CB	LEU	D	39	26.208	56.247	32.637	1.00	35.81	C
ATOM	2921	CG	LEU	D	39	24.706	56.030	32.689	1.00	34.18	C
ATOM	2922	CD1	LEU	D	39	24.285	56.206	34.141	1.00	33.76	C
ATOM	2923	CD2	LEU	D	39	23.900	56.980	31.827	1.00	31.66	C
ATOM	2924	N	PRO	D	40	28.807	57.926	31.852	1.00	44.17	N
ATOM	2925	CA	PRO	D	40	30.141	58.383	32.244	1.00	44.44	C
ATOM	2926	C	PRO	D	40	30.420	58.032	33.699	1.00	42.47	C
ATOM	2927	O	PRO	D	40	29.550	58.003	34.562	1.00	42.05	O
ATOM	2928	CB	PRO	D	40	30.115	59.908	32.011	1.00	45.14	C
ATOM	2929	CG	PRO	D	40	28.674	60.256	32.263	1.00	45.10	C
ATOM	2930	CD	PRO	D	40	27.934	59.092	31.603	1.00	46.22	C
ATOM	2931	N	SER	D	41	31.694	57.749	33.906	1.00	42.00	N
ATOM	2932	CA	SER	D	41	32.266	57.360	35.166	1.00	39.50	C
ATOM	2933	C	SER	D	41	31.724	58.115	36.365	1.00	38.61	C
ATOM	2934	O	SER	D	41	31.345	57.439	37.303	1.00	38.99	O
ATOM	2935	CB	SER	D	41	33.760	57.491	35.009	1.00	40.43	C
ATOM	2936	OG	SER	D	41	34.204	56.814	33.824	1.00	45.16	O
ATOM	2937	N	HIS	D	42	31.550	59.442	36.396	1.00	38.17	N
ATOM	2938	CA	HIS	D	42	31.018	60.127	37.567	1.00	36.99	C
ATOM	2939	C	HIS	D	42	29.633	59.685	38.068	1.00	38.51	C
ATOM	2940	O	HIS	D	42	29.219	59.978	39.190	1.00	39.73	O
ATOM	2941	CB	HIS	D	42	31.062	61.646	37.328	1.00	36.53	C
ATOM	2942	CG	HIS	D	42	29.988	62.146	36.370	1.00	34.40	C
ATOM	2943	ND1	HIS	D	42	30.070	62.275	35.063	1.00	35.82	N
ATOM	2944	CD2	HIS	D	42	28.694	62.443	36.749	1.00	36.22	C
ATOM	2945	CE1	HIS	D	42	28.872	62.607	34.629	1.00	35.92	C
ATOM	2946	NE2	HIS	D	42	28.050	62.680	35.644	1.00	37.56	N
ATOM	2947	N	CYS	D	43	28.848	58.974	37.261	1.00	40.38	N

Figure 8-60

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ATOM   2948  CA  CYS D  43      27.521  58.516  37.662  1.00 40.95           C
ATOM   2949  C   CYS D  43      27.545  57.165  38.394  1.00 38.66           C
ATOM   2950  O   CYS D  43      26.556  56.769  39.027  1.00 38.58           O
ATOM   2951  CB  CYS D  43      26.561  58.489  36.426  1.00 43.16           C
ATOM   2952  SG  CYS D  43      25.889  60.126  35.971  1.00 50.07           S
ATOM   2953  N   TRP D  44      28.677  56.450  38.300  1.00 34.96           N
ATOM   2954  CA  TRP D  44      28.763  55.094  38.789  1.00 32.27           C
ATOM   2955  C   TRP D  44      30.055  54.754  39.486  1.00 32.35           C
ATOM   2956  O   TRP D  44      30.010  53.891  40.349  1.00 34.30           O
ATOM   2957  CB  TRP D  44      28.502  54.045  37.688  1.00 29.74           C
ATOM   2958  CG  TRP D  44      29.428  54.039  36.479  1.00 25.62           C
ATOM   2959  CD1 TRP D  44      29.034  54.689  35.340  1.00 24.56           C
ATOM   2960  CD2 TRP D  44      30.636  53.392  36.360  1.00 24.29           C
ATOM   2961  NE1 TRP D  44      30.006  54.462  34.497  1.00 26.57           N
ATOM   2962  CE2 TRP D  44      30.972  53.705  35.046  1.00 25.16           C
ATOM   2963  CE3 TRP D  44      31.442  52.536  37.072  1.00 21.05           C
ATOM   2964  CZ2 TRP D  44      32.119  53.210  34.446  1.00 23.57           C
ATOM   2965  CZ3 TRP D  44      32.600  52.058  36.490  1.00 21.72           C
ATOM   2966  CH2 TRP D  44      32.956  52.395  35.194  1.00 23.72           C
ATOM   2967  N   ILE D  45      31.191  55.378  39.216  1.00 31.34           N
ATOM   2968  CA  ILE D  45      32.444  54.851  39.687  1.00 34.23           C
ATOM   2969  C   ILE D  45      32.627  54.719  41.206  1.00 35.04           C
ATOM   2970  O   ILE D  45      33.222  53.726  41.618  1.00 36.05           O
ATOM   2971  CB  ILE D  45      33.586  55.584  38.980  1.00 35.62           C
ATOM   2972  CG1 ILE D  45      34.959  54.917  39.068  1.00 36.05           C
ATOM   2973  CG2 ILE D  45      33.716  56.959  39.592  1.00 37.86           C
ATOM   2974  CD1 ILE D  45      35.020  53.482  38.545  1.00 36.81           C
ATOM   2975  N   SER D  46      32.100  55.591  42.080  1.00 35.07           N
ATOM   2976  CA  SER D  46      32.421  55.538  43.500  1.00 35.85           C
ATOM   2977  C   SER D  46      31.651  54.443  44.213  1.00 35.51           C
ATOM   2978  O   SER D  46      32.169  53.858  45.165  1.00 38.41           O
ATOM   2979  CB  SER D  46      32.165  56.852  44.223  1.00 36.96           C
ATOM   2980  OG  SER D  46      30.786  57.005  44.534  1.00 40.12           O
ATOM   2981  N   GLU D  47      30.419  54.185  43.770  1.00 33.93           N
ATOM   2982  CA  GLU D  47      29.656  53.051  44.230  1.00 32.65           C
ATOM   2983  C   GLU D  47      30.197  51.773  43.648  1.00 31.56           C
ATOM   2984  O   GLU D  47      30.216  50.761  44.339  1.00 31.25           O
ATOM   2985  CB  GLU D  47      28.206  53.193  43.842  1.00 36.42           C
ATOM   2986  CG  GLU D  47      27.306  51.989  44.164  1.00 45.32           C
ATOM   2987  CD  GLU D  47      26.964  51.716  45.628  1.00 48.90           C
ATOM   2988  OE1 GLU D  47      27.839  51.323  46.399  1.00 52.24           O
ATOM   2989  OE2 GLU D  47      25.797  51.872  45.995  1.00 52.95           O
HETATM 2990  N   MSE D  48      30.646  51.788  42.398  1.00 30.45           N
HETATM 2991  CA  MSE D  48      31.189  50.592  41.798  1.00 31.67           C
HETATM 2992  C   MSE D  48      32.499  50.155  42.444  1.00 30.88           C
HETATM 2993  O   MSE D  48      32.694  48.961  42.577  1.00 33.46           O
HETATM 2994  CB  MSE D  48      31.394  50.777  40.342  1.00 32.74           C
HETATM 2995  CG  MSE D  48      31.510  49.459  39.632  1.00 36.29           C
HETATM 2996  SE  MSE D  48      29.910  48.366  39.787  1.00 47.34          SE
HETATM 2997  CE  MSE D  48      30.895  46.927  39.264  1.00 38.75           C
ATOM   2998  N   VAL D  49      33.433  50.984  42.904  1.00 30.60           N
ATOM   2999  CA  VAL D  49      34.605  50.504  43.671  1.00 29.47           C
ATOM   3000  C   VAL D  49      34.285  50.012  45.074  1.00 27.89           C
ATOM   3001  O   VAL D  49      34.967  49.128  45.596  1.00 27.63           O
ATOM   3002  CB  VAL D  49      35.828  51.488  43.781  1.00 30.38           C
ATOM   3003  CG1 VAL D  49      36.552  51.617  42.439  1.00 30.57           C
ATOM   3004  CG2 VAL D  49      35.440  52.863  44.340  1.00 30.43           C
ATOM   3005  N   VAL D  50      33.263  50.622  45.679  1.00 25.21           N
ATOM   3006  CA  VAL D  50      32.754  50.149  46.945  1.00 24.70           C
ATOM   3007  C   VAL D  50      32.153  48.745  46.832  1.00 24.08           C
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Figure 8-61

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ATOM   3008  O   VAL D  50      32.438  47.921  47.699  1.00 25.08           O
ATOM   3009  CB  VAL D  50      31.757  51.172  47.504  1.00 24.15           C
ATOM   3010  CG1 VAL D  50      30.945  50.583  48.650  1.00 24.85           C
ATOM   3011  CG2 VAL D  50      32.484  52.411  47.974  1.00 21.01           C
ATOM   3012  N   GLN D  51      31.343  48.470  45.796  1.00 22.06           N
ATOM   3013  CA  GLN D  51      30.807  47.154  45.522  1.00 22.13           C
ATOM   3014  C   GLN D  51      31.810  46.099  45.123  1.00 20.89           C
ATOM   3015  O   GLN D  51      31.663  44.940  45.479  1.00 21.33           O
ATOM   3016  CB  GLN D  51      29.719  47.249  44.484  1.00 24.57           C
ATOM   3017  CG  GLN D  51      28.496  47.999  45.018  1.00 26.12           C
ATOM   3018  CD  GLN D  51      27.936  47.379  46.304  1.00 26.75           C
ATOM   3019  OE1 GLN D  51      28.128  46.194  46.616  1.00 25.54           O
ATOM   3020  NE2 GLN D  51      27.234  48.198  47.088  1.00 26.23           N
ATOM   3021  N   LEU D  52      32.839  46.544  44.423  1.00 19.69           N
ATOM   3022  CA  LEU D  52      33.966  45.728  44.057  1.00 20.34           C
ATOM   3023  C   LEU D  52      34.831  45.383  45.250  1.00 20.47           C
ATOM   3024  O   LEU D  52      35.199  44.215  45.356  1.00 23.75           O
ATOM   3025  CB  LEU D  52      34.866  46.398  42.976  1.00 19.72           C
ATOM   3026  CG  LEU D  52      34.402  46.541  41.509  1.00 18.02           C
ATOM   3027  CD1 LEU D  52      35.404  47.412  40.807  1.00 14.47           C
ATOM   3028  CD2 LEU D  52      34.217  45.177  40.844  1.00 14.93           C
ATOM   3029  N   SER D  53      35.178  46.294  46.165  1.00 21.36           N
ATOM   3030  CA  SER D  53      35.913  45.942  47.377  1.00 22.45           C
ATOM   3031  C   SER D  53      35.173  44.873  48.166  1.00 22.70           C
ATOM   3032  O   SER D  53      35.770  43.895  48.565  1.00 24.55           O
ATOM   3033  CB  SER D  53      36.117  47.178  48.233  1.00 25.43           C
ATOM   3034  OG  SER D  53      36.882  46.917  49.410  1.00 32.17           O
ATOM   3035  N   ASP D  54      33.852  44.962  48.286  1.00 23.74           N
ATOM   3036  CA  ASP D  54      33.021  44.038  49.030  1.00 25.51           C
ATOM   3037  C   ASP D  54      33.119  42.633  48.500  1.00 22.56           C
ATOM   3038  O   ASP D  54      33.390  41.711  49.250  1.00 22.33           O
ATOM   3039  CB  ASP D  54      31.565  44.500  48.963  1.00 32.00           C
ATOM   3040  CG  ASP D  54      30.624  43.913  50.019  1.00 42.23           C
ATOM   3041  OD1 ASP D  54      30.117  42.792  49.841  1.00 45.21           O
ATOM   3042  OD2 ASP D  54      30.364  44.607  51.018  1.00 49.94           O
ATOM   3043  N   SER D  55      32.943  42.520  47.192  1.00 19.99           N
ATOM   3044  CA  SER D  55      32.933  41.258  46.504  1.00 16.42           C
ATOM   3045  C   SER D  55      34.279  40.596  46.521  1.00 14.71           C
ATOM   3046  O   SER D  55      34.395  39.393  46.693  1.00 15.83           O
ATOM   3047  CB  SER D  55      32.503  41.468  45.066  1.00 16.29           C
ATOM   3048  OG  SER D  55      31.170  41.909  44.886  1.00 19.97           O
ATOM   3049  N   LEU D  56      35.296  41.408  46.315  1.00 15.85           N
ATOM   3050  CA  LEU D  56      36.638  40.884  46.345  1.00 17.57           C
ATOM   3051  C   LEU D  56      37.034  40.485  47.744  1.00 17.75           C
ATOM   3052  O   LEU D  56      37.782  39.527  47.863  1.00 19.01           O
ATOM   3053  CB  LEU D  56      37.619  41.904  45.848  1.00 17.61           C
ATOM   3054  CG  LEU D  56      37.813  42.091  44.344  1.00 21.27           C
ATOM   3055  CD1 LEU D  56      38.577  43.396  44.141  1.00 19.96           C
ATOM   3056  CD2 LEU D  56      38.540  40.936  43.687  1.00 16.32           C
ATOM   3057  N   THR D  57      36.560  41.169  48.803  1.00 19.07           N
ATOM   3058  CA  THR D  57      36.864  40.818  50.189  1.00 17.97           C
ATOM   3059  C   THR D  57      36.126  39.571  50.566  1.00 18.20           C
ATOM   3060  O   THR D  57      36.674  38.746  51.266  1.00 20.89           O
ATOM   3061  CB  THR D  57      36.521  41.984  51.099  1.00 19.37           C
ATOM   3062  OG1 THR D  57      37.503  42.932  50.741  1.00 20.91           O
ATOM   3063  CG2 THR D  57      36.778  41.786  52.575  1.00 26.13           C
ATOM   3064  N   ASP D  58      34.924  39.346  50.085  1.00 18.03           N
ATOM   3065  CA  ASP D  58      34.293  38.066  50.220  1.00 18.76           C
ATOM   3066  C   ASP D  58      34.958  37.009  49.397  1.00 20.46           C
ATOM   3067  O   ASP D  58      35.041  35.878  49.865  1.00 20.47           O
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Figure 8-62

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ATOM   3068  CB  ASP D  58      32.859  38.102  49.791  1.00 21.24           C
ATOM   3069  CG  ASP D  58      32.043  39.157  50.517  1.00 26.19           C
ATOM   3070  OD1 ASP D  58      32.458  39.665  51.572  1.00 26.83           O
ATOM   3071  OD2 ASP D  58      30.970  39.481  49.993  1.00 30.50           O
ATOM   3072  N   LEU D  59      35.449  37.324  48.197  1.00 19.65           N
ATOM   3073  CA  LEU D  59      36.099  36.331  47.383  1.00 18.09           C
ATOM   3074  C   LEU D  59      37.345  35.878  48.090  1.00 19.12           C
ATOM   3075  O   LEU D  59      37.553  34.694  48.251  1.00 23.04           O
ATOM   3076  CB  LEU D  59      36.392  36.893  46.028  1.00 16.75           C
ATOM   3077  CG  LEU D  59      36.808  35.864  45.048  1.00 17.14           C
ATOM   3078  CD1 LEU D  59      35.714  34.823  44.909  1.00 16.41           C
ATOM   3079  CD2 LEU D  59      37.209  36.546  43.769  1.00 16.93           C
ATOM   3080  N   LEU D  60      38.132  36.764  48.667  1.00 21.47           N
ATOM   3081  CA  LEU D  60      39.332  36.428  49.431  1.00 22.73           C
ATOM   3082  C   LEU D  60      39.173  35.401  50.564  1.00 24.38           C
ATOM   3083  O   LEU D  60      40.084  34.626  50.853  1.00 25.12           O
ATOM   3084  CB  LEU D  60      39.852  37.726  50.017  1.00 21.70           C
ATOM   3085  CG  LEU D  60      41.196  37.710  50.670  1.00 23.77           C
ATOM   3086  CD1 LEU D  60      42.256  37.514  49.598  1.00 22.63           C
ATOM   3087  CD2 LEU D  60      41.446  38.985  51.425  1.00 24.99           C
ATOM   3088  N   ASP D  61      38.005  35.386  51.224  1.00 26.63           N
ATOM   3089  CA  ASP D  61      37.705  34.524  52.363  1.00 25.59           C
ATOM   3090  C   ASP D  61      37.428  33.112  51.872  1.00 22.43           C
ATOM   3091  O   ASP D  61      37.373  32.161  52.646  1.00 23.39           O
ATOM   3092  CB  ASP D  61      36.497  35.146  53.120  1.00 33.33           C
ATOM   3093  CG  ASP D  61      35.889  34.390  54.325  1.00 40.36           C
ATOM   3094  OD1 ASP D  61      36.478  34.403  55.424  1.00 44.78           O
ATOM   3095  OD2 ASP D  61      34.807  33.794  54.169  1.00 43.10           O
ATOM   3096  N   LYS D  62      37.289  32.899  50.575  1.00 17.94           N
ATOM   3097  CA  LYS D  62      37.048  31.574  50.058  1.00 13.29           C
ATOM   3098  C   LYS D  62      38.344  30.855  49.757  1.00 12.68           C
ATOM   3099  O   LYS D  62      38.308  29.692  49.387  1.00 15.69           O
ATOM   3100  CB  LYS D  62      36.292  31.712  48.771  1.00 13.99           C
ATOM   3101  CG  LYS D  62      35.036  32.517  48.890  1.00 16.25           C
ATOM   3102  CD  LYS D  62      34.086  31.871  49.870  1.00 21.21           C
ATOM   3103  CE  LYS D  62      32.997  32.898  50.166  1.00 23.50           C
ATOM   3104  NZ  LYS D  62      32.319  33.267  48.937  1.00 30.45           N
ATOM   3105  N   PHE D  63      39.504  31.504  49.885  1.00 12.18           N
ATOM   3106  CA  PHE D  63      40.797  30.938  49.594  1.00 13.29           C
ATOM   3107  C   PHE D  63      41.659  30.965  50.837  1.00 16.38           C
ATOM   3108  O   PHE D  63      41.401  31.701  51.798  1.00 16.40           O
ATOM   3109  CB  PHE D  63      41.495  31.773  48.552  1.00 11.01           C
ATOM   3110  CG  PHE D  63      40.776  31.641  47.229  1.00 13.33           C
ATOM   3111  CD1 PHE D  63      40.917  30.478  46.491  1.00 11.26           C
ATOM   3112  CD2 PHE D  63      39.904  32.635  46.823  1.00 13.18           C
ATOM   3113  CE1 PHE D  63      40.140  30.299  45.367  1.00  9.84           C
ATOM   3114  CE2 PHE D  63      39.126  32.436  45.690  1.00 13.90           C
ATOM   3115  CZ  PHE D  63      39.251  31.264  44.964  1.00 10.53           C
ATOM   3116  N   SER D  64      42.725  30.164  50.773  1.00 16.82           N
ATOM   3117  CA  SER D  64      43.703  30.208  51.822  1.00 16.74           C
ATOM   3118  C   SER D  64      45.123  30.230  51.275  1.00 16.89           C
ATOM   3119  O   SER D  64      45.377  29.918  50.120  1.00 16.97           O
ATOM   3120  CB  SER D  64      43.430  29.068  52.849  1.00 18.93           C
ATOM   3121  OG  SER D  64      44.080  27.847  52.508  1.00 28.04           O
ATOM   3122  N   ASN D  65      46.080  30.661  52.095  1.00 16.96           N
ATOM   3123  CA  ASN D  65      47.479  30.684  51.746  1.00 15.98           C
ATOM   3124  C   ASN D  65      48.027  29.319  51.496  1.00 15.15           C
ATOM   3125  O   ASN D  65      47.472  28.362  52.000  1.00 17.07           O
ATOM   3126  CB  ASN D  65      48.341  31.398  52.774  1.00 17.48           C
ATOM   3127  CG  ASN D  65      48.232  32.904  52.684  1.00 19.71           C
```

Figure 8-63

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ATOM   3128  OD1 ASN D  65      48.695  33.551  51.752  1.00 25.73           O
ATOM   3129  ND2 ASN D  65      47.621  33.560  53.640  1.00 22.21           N
ATOM   3130  N   ILE D  66      49.077  29.253  50.672  1.00 15.61           N
ATOM   3131  CA  ILE D  66      49.778  28.029  50.363  1.00 16.53           C
ATOM   3132  C   ILE D  66      51.232  28.235  50.711  1.00 16.49           C
ATOM   3133  O   ILE D  66      51.633  29.383  50.813  1.00 17.79           O
ATOM   3134  CB  ILE D  66      49.594  27.623  48.869  1.00 16.19           C
ATOM   3135  CG1 ILE D  66      50.149  28.660  47.906  1.00 16.66           C
ATOM   3136  CG2 ILE D  66      48.115  27.329  48.611  1.00 12.63           C
ATOM   3137  CD1 ILE D  66      50.081  28.086  46.478  1.00 18.10           C
ATOM   3138  N   SER D  67      52.041  27.187  50.853  1.00 18.84           N
ATOM   3139  CA  SER D  67      53.442  27.347  51.233  1.00 23.17           C
ATOM   3140  C   SER D  67      54.305  28.078  50.214  1.00 23.34           C
ATOM   3141  O   SER D  67      55.250  28.779  50.552  1.00 25.92           O
ATOM   3142  CB  SER D  67      54.084  26.006  51.543  1.00 23.00           C
ATOM   3143  OG  SER D  67      53.971  25.139  50.419  1.00 30.06           O
ATOM   3144  N   GLU D  68      53.981  27.968  48.942  1.00 25.32           N
ATOM   3145  CA  GLU D  68      54.755  28.626  47.914  1.00 27.08           C
ATOM   3146  C   GLU D  68      54.045  28.401  46.597  1.00 25.08           C
ATOM   3147  O   GLU D  68      53.391  27.373  46.403  1.00 24.26           O
ATOM   3148  CB  GLU D  68      56.190  28.061  47.921  1.00 30.32           C
ATOM   3149  CG  GLU D  68      56.711  27.081  46.883  1.00 40.98           C
ATOM   3150  CD  GLU D  68      56.009  25.744  46.778  1.00 46.80           C
ATOM   3151  OE1 GLU D  68      55.947  24.998  47.773  1.00 50.12           O
ATOM   3152  OE2 GLU D  68      55.508  25.470  45.676  1.00 52.68           O
ATOM   3153  N   GLY D  69      54.121  29.389  45.723  1.00 23.65           N
ATOM   3154  CA  GLY D  69      53.784  29.192  44.320  1.00 24.95           C
ATOM   3155  C   GLY D  69      52.580  30.012  43.952  1.00 23.05           C
ATOM   3156  O   GLY D  69      52.270  30.941  44.691  1.00 24.04           O
ATOM   3157  N   LEU D  70      51.883  29.667  42.870  1.00 22.75           N
ATOM   3158  CA  LEU D  70      50.768  30.474  42.415  1.00 23.31           C
ATOM   3159  C   LEU D  70      49.618  30.380  43.412  1.00 21.85           C
ATOM   3160  O   LEU D  70      49.170  29.262  43.689  1.00 23.27           O
ATOM   3161  CB  LEU D  70      50.307  29.902  41.114  1.00 22.88           C
ATOM   3162  CG  LEU D  70      49.652  30.850  40.145  1.00 22.31           C
ATOM   3163  CD1 LEU D  70      49.073  29.925  39.088  1.00 24.98           C
ATOM   3164  CD2 LEU D  70      48.576  31.722  40.710  1.00 21.90           C
ATOM   3165  N   SER D  71      49.143  31.526  43.918  1.00 19.05           N
ATOM   3166  CA  SER D  71      48.132  31.561  44.977  1.00 16.36           C
ATOM   3167  C   SER D  71      47.008  32.518  44.667  1.00 15.90           C
ATOM   3168  O   SER D  71      47.262  33.701  44.521  1.00 18.19           O
ATOM   3169  CB  SER D  71      48.747  32.015  46.298  1.00 15.26           C
ATOM   3170  OG  SER D  71      47.822  32.217  47.360  1.00 16.34           O
ATOM   3171  N   ASN D  72      45.757  32.053  44.598  1.00 17.24           N
ATOM   3172  CA  ASN D  72      44.604  32.871  44.335  1.00 14.30           C
ATOM   3173  C   ASN D  72      44.451  33.836  45.493  1.00 16.33           C
ATOM   3174  O   ASN D  72      44.170  35.023  45.286  1.00 16.94           O
ATOM   3175  CB  ASN D  72      43.399  31.967  44.208  1.00 14.51           C
ATOM   3176  CG  ASN D  72      43.311  31.102  42.953  1.00 14.36           C
ATOM   3177  OD1 ASN D  72      44.170  31.156  42.089  1.00 15.41           O
ATOM   3178  ND2 ASN D  72      42.291  30.261  42.779  1.00 14.10           N
ATOM   3179  N   TYR D  73      44.711  33.348  46.720  1.00 16.70           N
ATOM   3180  CA  TYR D  73      44.709  34.222  47.893  1.00 17.86           C
ATOM   3181  C   TYR D  73      45.580  35.466  47.698  1.00 17.22           C
ATOM   3182  O   TYR D  73      45.047  36.559  47.813  1.00 19.51           O
ATOM   3183  CB  TYR D  73      45.171  33.479  49.182  1.00 15.83           C
ATOM   3184  CG  TYR D  73      44.962  34.331  50.421  1.00 11.11           C
ATOM   3185  CD1 TYR D  73      43.755  34.297  51.064  1.00 13.95           C
ATOM   3186  CD2 TYR D  73      45.932  35.212  50.823  1.00 14.63           C
ATOM   3187  CE1 TYR D  73      43.474  35.184  52.080  1.00 15.34           C
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Figure 8-64

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ATOM   3188  CE2 TYR D  73      45.663  36.140  51.814  1.00 15.34           C
ATOM   3189  CZ  TYR D  73      44.430  36.108  52.407  1.00 16.30           C
ATOM   3190  OH  TYR D  73      44.123  37.051  53.334  1.00 22.01           O
ATOM   3191  N   SER D  74      46.888  35.357  47.402  1.00 18.57           N
ATOM   3192  CA  SER D  74      47.786  36.498  47.221  1.00 17.90           C
ATOM   3193  C   SER D  74      47.420  37.417  46.121  1.00 16.44           C
ATOM   3194  O   SER D  74      47.636  38.600  46.291  1.00 18.01           O
ATOM   3195  CB  SER D  74      49.180  36.125  46.829  1.00 18.93           C
ATOM   3196  OG  SER D  74      49.623  35.176  47.760  1.00 25.77           O
ATOM   3197  N   ILE D  75      46.890  36.866  45.027  1.00 16.68           N
ATOM   3198  CA  ILE D  75      46.470  37.645  43.893  1.00 16.88           C
ATOM   3199  C   ILE D  75      45.256  38.493  44.244  1.00 16.78           C
ATOM   3200  O   ILE D  75      45.237  39.693  43.968  1.00 20.42           O
ATOM   3201  CB  ILE D  75      46.184  36.709  42.711  1.00 16.41           C
ATOM   3202  CG1 ILE D  75      47.380  35.898  42.295  1.00 16.78           C
ATOM   3203  CG2 ILE D  75      45.861  37.615  41.567  1.00 16.46           C
ATOM   3204  CD1 ILE D  75      47.146  34.967  41.097  1.00 19.66           C
ATOM   3205  N   ILE D  76      44.230  37.936  44.901  1.00 18.21           N
ATOM   3206  CA  ILE D  76      43.023  38.678  45.220  1.00 15.41           C
ATOM   3207  C   ILE D  76      43.340  39.669  46.286  1.00 17.60           C
ATOM   3208  O   ILE D  76      42.870  40.796  46.215  1.00 20.17           O
ATOM   3209  CB  ILE D  76      41.941  37.743  45.711  1.00 16.42           C
ATOM   3210  CG1 ILE D  76      41.615  36.789  44.588  1.00 14.92           C
ATOM   3211  CG2 ILE D  76      40.696  38.481  46.200  1.00 11.21           C
ATOM   3212  CD1 ILE D  76      40.745  35.613  45.055  1.00 13.69           C
ATOM   3213  N   ASP D  77      44.162  39.271  47.248  1.00 19.35           N
ATOM   3214  CA  ASP D  77      44.561  40.150  48.321  1.00 21.77           C
ATOM   3215  C   ASP D  77      45.248  41.436  47.858  1.00 22.56           C
ATOM   3216  O   ASP D  77      44.924  42.515  48.376  1.00 22.07           O
ATOM   3217  CB  ASP D  77      45.433  39.385  49.282  1.00 24.17           C
ATOM   3218  CG  ASP D  77      45.713  40.148  50.571  1.00 28.55           C
ATOM   3219  OD1 ASP D  77      44.842  40.889  51.067  1.00 33.63           O
ATOM   3220  OD2 ASP D  77      46.822  39.988  51.073  1.00 28.53           O
ATOM   3221  N   LYS D  78      46.139  41.344  46.851  1.00 22.27           N
ATOM   3222  CA  LYS D  78      46.692  42.534  46.222  1.00 21.32           C
ATOM   3223  C   LYS D  78      45.654  43.318  45.471  1.00 19.56           C
ATOM   3224  O   LYS D  78      45.786  44.524  45.417  1.00 22.75           O
ATOM   3225  CB  LYS D  78      47.807  42.270  45.230  1.00 23.87           C
ATOM   3226  CG  LYS D  78      49.036  41.600  45.795  1.00 30.71           C
ATOM   3227  CD  LYS D  78      50.269  41.917  44.947  1.00 37.30           C
ATOM   3228  CE  LYS D  78      51.317  40.799  45.004  1.00 40.34           C
ATOM   3229  NZ  LYS D  78      50.843  39.671  44.214  1.00 44.85           N
ATOM   3230  N   LEU D  79      44.634  42.714  44.882  1.00 18.00           N
ATOM   3231  CA  LEU D  79      43.570  43.462  44.247  1.00 16.42           C
ATOM   3232  C   LEU D  79      42.696  44.124  45.273  1.00 18.98           C
ATOM   3233  O   LEU D  79      42.215  45.218  45.035  1.00 21.86           O
ATOM   3234  CB  LEU D  79      42.687  42.543  43.451  1.00 13.71           C
ATOM   3235  CG  LEU D  79      43.383  41.746  42.358  1.00 13.81           C
ATOM   3236  CD1 LEU D  79      42.294  41.091  41.522  1.00 14.16           C
ATOM   3237  CD2 LEU D  79      44.240  42.627  41.462  1.00 11.49           C
ATOM   3238  N   VAL D  80      42.438  43.524  46.430  1.00 19.01           N
ATOM   3239  CA  VAL D  80      41.624  44.124  47.462  1.00 20.11           C
ATOM   3240  C   VAL D  80      42.369  45.343  47.920  1.00 21.57           C
ATOM   3241  O   VAL D  80      41.759  46.389  47.987  1.00 25.14           O
ATOM   3242  CB  VAL D  80      41.480  43.093  48.603  1.00 22.94           C
ATOM   3243  CG1 VAL D  80      40.920  43.647  49.896  1.00 25.85           C
ATOM   3244  CG2 VAL D  80      40.511  42.003  48.246  1.00 20.39           C
ATOM   3245  N   ASN D  81      43.678  45.313  48.167  1.00 24.08           N
ATOM   3246  CA  ASN D  81      44.375  46.498  48.626  1.00 23.59           C
ATOM   3247  C   ASN D  81      44.363  47.632  47.620  1.00 26.17           C
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Figure 8-65

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ATOM   3248  O   ASN D  81      44.334  48.756  48.114  1.00 28.26           O
ATOM   3249  CB  ASN D  81      45.761  46.180  49.097  1.00 21.14           C
ATOM   3250  CG  ASN D  81      45.684  45.257  50.278  1.00 23.73           C
ATOM   3251  OD1 ASN D  81      44.871  45.422  51.175  1.00 31.16           O
ATOM   3252  ND2 ASN D  81      46.490  44.231  50.357  1.00 25.26           N
ATOM   3253  N   ILE D  82      44.340  47.414  46.280  1.00 25.02           N
ATOM   3254  CA  ILE D  82      44.088  48.469  45.268  1.00 25.82           C
ATOM   3255  C   ILE D  82      42.671  49.103  45.287  1.00 25.89           C
ATOM   3256  O   ILE D  82      42.512  50.323  45.196  1.00 25.87           O
ATOM   3257  CB  ILE D  82      44.444  48.002  43.847  1.00 23.39           C
ATOM   3258  CG1 ILE D  82      45.885  47.557  43.751  1.00 25.26           C
ATOM   3259  CG2 ILE D  82      44.317  49.150  42.894  1.00 23.94           C
ATOM   3260  CD1 ILE D  82      46.185  46.717  42.500  1.00 24.24           C
ATOM   3261  N   VAL D  83      41.595  48.324  45.443  1.00 27.50           N
ATOM   3262  CA  VAL D  83      40.240  48.859  45.486  1.00 27.69           C
ATOM   3263  C   VAL D  83      40.017  49.556  46.841  1.00 30.42           C
ATOM   3264  O   VAL D  83      39.190  50.454  46.938  1.00 29.44           O
ATOM   3265  CB  VAL D  83      39.230  47.758  45.201  1.00 23.07           C
ATOM   3266  CG1 VAL D  83      37.910  48.384  44.868  1.00 24.95           C
ATOM   3267  CG2 VAL D  83      39.634  47.000  43.979  1.00 23.59           C
ATOM   3268  N   ASP D  84      40.772  49.192  47.892  1.00 32.89           N
ATOM   3269  CA  ASP D  84      40.753  49.840  49.206  1.00 35.85           C
ATOM   3270  C   ASP D  84      41.361  51.238  49.084  1.00 35.75           C
ATOM   3271  O   ASP D  84      40.779  52.212  49.557  1.00 35.62           O
ATOM   3272  CB  ASP D  84      41.531  49.029  50.294  1.00 39.03           C
ATOM   3273  CG  ASP D  84      40.827  48.006  51.221  1.00 41.67           C
ATOM   3274  OD1 ASP D  84      39.593  47.858  51.172  1.00 43.23           O
ATOM   3275  OD2 ASP D  84      41.536  47.352  52.008  1.00 43.54           O
ATOM   3276  N   ASP D  85      42.500  51.382  48.417  1.00 35.24           N
ATOM   3277  CA  ASP D  85      43.039  52.689  48.095  1.00 39.54           C
ATOM   3278  C   ASP D  85      42.055  53.620  47.372  1.00 40.48           C
ATOM   3279  O   ASP D  85      41.712  54.706  47.853  1.00 42.05           O
ATOM   3280  CB  ASP D  85      44.343  52.540  47.287  1.00 41.18           C
ATOM   3281  CG  ASP D  85      45.534  51.871  48.001  1.00 43.42           C
ATOM   3282  OD1 ASP D  85      45.537  51.723  49.243  1.00 41.35           O
ATOM   3283  OD2 ASP D  85      46.465  51.488  47.276  1.00 42.78           O
ATOM   3284  N   LEU D  86      41.518  53.157  46.238  1.00 41.90           N
ATOM   3285  CA  LEU D  86      40.526  53.903  45.456  1.00 39.57           C
ATOM   3286  C   LEU D  86      39.249  54.172  46.203  1.00 38.81           C
ATOM   3287  O   LEU D  86      38.614  55.176  45.924  1.00 40.16           O
ATOM   3288  CB  LEU D  86      40.142  53.164  44.191  1.00 36.00           C
ATOM   3289  CG  LEU D  86      41.234  52.732  43.251  1.00 34.91           C
ATOM   3290  CD1 LEU D  86      40.618  52.075  42.047  1.00 33.95           C
ATOM   3291  CD2 LEU D  86      42.096  53.907  42.858  1.00 32.40           C
ATOM   3292  N   VAL D  87      38.840  53.303  47.125  1.00 40.82           N
ATOM   3293  CA  VAL D  87      37.680  53.589  47.958  1.00 44.87           C
ATOM   3294  C   VAL D  87      37.965  54.754  48.933  1.00 47.95           C
ATOM   3295  O   VAL D  87      37.085  55.580  49.176  1.00 49.04           O
ATOM   3296  CB  VAL D  87      37.191  52.311  48.682  1.00 42.48           C
ATOM   3297  CG1 VAL D  87      36.094  52.685  49.647  1.00 43.30           C
ATOM   3298  CG2 VAL D  87      36.572  51.285  47.749  1.00 39.59           C
ATOM   3299  N   GLU D  88      39.185  54.862  49.472  1.00 51.32           N
ATOM   3300  CA  GLU D  88      39.548  55.935  50.387  1.00 55.88           C
ATOM   3301  C   GLU D  88      39.807  57.235  49.672  1.00 57.32           C
ATOM   3302  O   GLU D  88      39.717  58.303  50.291  1.00 59.78           O
ATOM   3303  CB  GLU D  88      40.786  55.627  51.225  1.00 57.84           C
ATOM   3304  CG  GLU D  88      40.534  54.935  52.572  1.00 61.46           C
ATOM   3305  CD  GLU D  88      41.737  54.106  53.056  1.00 65.66           C
ATOM   3306  OE1 GLU D  88      42.872  54.610  53.000  1.00 65.91           O
ATOM   3307  OE2 GLU D  88      41.543  52.947  53.479  1.00 68.20           O
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Figure 8-66

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ATOM   3308  N   CYS D  89      40.147  57.130  48.382  1.00 57.61           N
ATOM   3309  CA  CYS D  89      40.273  58.307  47.528  1.00 58.46           C
ATOM   3310  C   CYS D  89      38.895  58.970  47.344  1.00 58.39           C
ATOM   3311  O   CYS D  89      38.791  60.197  47.378  1.00 58.21           O
ATOM   3312  CB  CYS D  89      40.931  57.880  46.221  1.00 57.54           C
ATOM   3313  SG  CYS D  89      41.341  59.181  45.038  1.00 58.90           S
ATOM   3314  N   VAL D  90      37.809  58.179  47.271  1.00 58.70           N
ATOM   3315  CA  VAL D  90      36.453  58.684  47.150  1.00 59.63           C
ATOM   3316  C   VAL D  90      35.871  59.210  48.484  1.00 61.73           C
ATOM   3317  O   VAL D  90      34.680  59.004  48.763  1.00 62.80           O
ATOM   3318  CB  VAL D  90      35.602  57.544  46.539  1.00 58.55           C
ATOM   3319  N   SER D 104      20.665  52.244  45.909  1.00 56.19           N
ATOM   3320  CA  SER D 104      21.629  51.156  45.958  1.00 53.75           C
ATOM   3321  C   SER D 104      21.476  50.204  44.750  1.00 51.69           C
ATOM   3322  O   SER D 104      20.519  50.365  43.954  1.00 53.93           O
ATOM   3323  CB  SER D 104      21.454  50.421  47.297  1.00 55.38           C
ATOM   3324  OG  SER D 104      22.506  49.503  47.610  1.00 56.37           O
ATOM   3325  N   PRO D 105      22.446  49.277  44.526  1.00 45.68           N
ATOM   3326  CA  PRO D 105      22.366  48.292  43.470  1.00 41.30           C
ATOM   3327  C   PRO D 105      22.138  46.887  43.955  1.00 37.99           C
ATOM   3328  O   PRO D 105      22.529  46.478  45.049  1.00 38.93           O
ATOM   3329  CB  PRO D 105      23.661  48.481  42.741  1.00 40.55           C
ATOM   3330  CG  PRO D 105      24.631  48.664  43.862  1.00 42.00           C
ATOM   3331  CD  PRO D 105      23.856  49.476  44.863  1.00 42.72           C
ATOM   3332  N   GLU D 106      21.459  46.177  43.075  1.00 33.70           N
ATOM   3333  CA  GLU D 106      20.971  44.880  43.417  1.00 32.02           C
ATOM   3334  C   GLU D 106      21.976  43.812  43.085  1.00 32.36           C
ATOM   3335  O   GLU D 106      22.715  43.942  42.111  1.00 32.37           O
ATOM   3336  CB  GLU D 106      19.734  44.553  42.624  1.00 32.57           C
ATOM   3337  N   PRO D 107      22.006  42.732  43.886  1.00 32.45           N
ATOM   3338  CA  PRO D 107      22.855  41.549  43.686  1.00 31.86           C
ATOM   3339  C   PRO D 107      22.724  40.845  42.340  1.00 29.45           C
ATOM   3340  O   PRO D 107      21.623  40.491  41.911  1.00 29.62           O
ATOM   3341  CB  PRO D 107      22.403  40.614  44.801  1.00 32.83           C
ATOM   3342  CG  PRO D 107      22.040  41.574  45.904  1.00 34.59           C
ATOM   3343  CD  PRO D 107      21.299  42.658  45.165  1.00 31.98           C
ATOM   3344  N   ARG D 108      23.893  40.580  41.745  1.00 27.04           N
ATOM   3345  CA  ARG D 108      23.966  39.882  40.479  1.00 24.37           C
ATOM   3346  C   ARG D 108      25.090  38.834  40.442  1.00 22.83           C
ATOM   3347  O   ARG D 108      26.084  39.002  41.124  1.00 21.26           O
ATOM   3348  CB  ARG D 108      24.090  40.981  39.431  1.00 27.20           C
ATOM   3349  CG  ARG D 108      23.924  40.490  38.015  1.00 32.52           C
ATOM   3350  CD  ARG D 108      23.488  41.587  37.061  1.00 35.27           C
ATOM   3351  NE  ARG D 108      23.846  41.160  35.712  1.00 38.19           N
ATOM   3352  CZ  ARG D 108      23.536  41.872  34.627  1.00 38.97           C
ATOM   3353  NH1 ARG D 108      22.798  43.008  34.720  1.00 34.64           N
ATOM   3354  NH2 ARG D 108      23.995  41.398  33.454  1.00 39.61           N
ATOM   3355  N   LEU D 109      24.984  37.734  39.681  1.00 21.95           N
ATOM   3356  CA  LEU D 109      25.996  36.697  39.565  1.00 20.44           C
ATOM   3357  C   LEU D 109      26.760  36.756  38.265  1.00 18.72           C
ATOM   3358  O   LEU D 109      26.191  36.725  37.175  1.00 19.50           O
ATOM   3359  CB  LEU D 109      25.392  35.304  39.657  1.00 21.02           C
ATOM   3360  CG  LEU D 109      24.434  34.885  40.779  1.00 23.43           C
ATOM   3361  CD1 LEU D 109      24.170  33.404  40.648  1.00 24.08           C
ATOM   3362  CD2 LEU D 109      24.939  35.187  42.193  1.00 25.25           C
ATOM   3363  N   PHE D 110      28.080  36.753  38.437  1.00 17.94           N
ATOM   3364  CA  PHE D 110      29.031  36.804  37.333  1.00 17.25           C
ATOM   3365  C   PHE D 110      30.013  35.649  37.346  1.00 16.87           C
ATOM   3366  O   PHE D 110      30.417  35.198  38.404  1.00 19.49           O
ATOM   3367  CB  PHE D 110      29.848  38.070  37.366  1.00 16.08           C
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Figure 8-67

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ATOM   3368  CG  PHE D 110      28.993  39.305  37.265  1.00 18.38           C
ATOM   3369  CD1 PHE D 110      28.573  39.743  36.029  1.00 19.11           C
ATOM   3370  CD2 PHE D 110      28.633  39.977  38.408  1.00 16.78           C
ATOM   3371  CE1 PHE D 110      27.802  40.874  35.946  1.00 16.73           C
ATOM   3372  CE2 PHE D 110      27.850  41.103  38.321  1.00 18.17           C
ATOM   3373  CZ  PHE D 110      27.445  41.553  37.081  1.00 21.53           C
ATOM   3374  N   THR D 111      30.425  35.107  36.216  1.00 15.24           N
ATOM   3375  CA  THR D 111      31.539  34.192  36.176  1.00 14.72           C
ATOM   3376  C   THR D 111      32.811  34.994  36.443  1.00 12.40           C
ATOM   3377  O   THR D 111      32.752  36.218  36.400  1.00 13.27           O
ATOM   3378  CB  THR D 111      31.579  33.435  34.828  1.00 17.12           C
ATOM   3379  OG1 THR D 111      31.630  34.415  33.809  1.00 17.68           O
ATOM   3380  CG2 THR D 111      30.451  32.446  34.621  1.00 14.81           C
ATOM   3381  N   PRO D 112      33.974  34.412  36.757  1.00 12.31           N
ATOM   3382  CA  PRO D 112      35.219  35.126  36.935  1.00 11.10           C
ATOM   3383  C   PRO D 112      35.594  36.046  35.783  1.00 14.02           C
ATOM   3384  O   PRO D 112      35.884  37.215  36.011  1.00 13.17           O
ATOM   3385  CB  PRO D 112      36.189  33.965  37.074  1.00  9.39           C
ATOM   3386  CG  PRO D 112      35.413  32.952  37.854  1.00  7.72           C
ATOM   3387  CD  PRO D 112      34.151  32.972  37.061  1.00 11.01           C
ATOM   3388  N   GLU D 113      35.611  35.572  34.517  1.00 16.22           N
ATOM   3389  CA  GLU D 113      35.905  36.456  33.395  1.00 16.17           C
ATOM   3390  C   GLU D 113      35.026  37.679  33.272  1.00 13.99           C
ATOM   3391  O   GLU D 113      35.508  38.761  32.985  1.00 15.09           O
ATOM   3392  CB  GLU D 113      35.913  35.703  32.092  1.00 17.91           C
ATOM   3393  CG  GLU D 113      34.636  34.985  31.713  1.00 19.43           C
ATOM   3394  CD  GLU D 113      34.621  34.539  30.277  1.00 22.34           C
ATOM   3395  OE1 GLU D 113      35.652  34.599  29.608  1.00 23.91           O
ATOM   3396  OE2 GLU D 113      33.558  34.139  29.810  1.00 24.64           O
ATOM   3397  N   GLU D 114      33.747  37.539  33.559  1.00 14.85           N
ATOM   3398  CA  GLU D 114      32.837  38.649  33.596  1.00 15.81           C
ATOM   3399  C   GLU D 114      33.063  39.567  34.769  1.00 15.50           C
ATOM   3400  O   GLU D 114      33.085  40.783  34.557  1.00 15.87           O
ATOM   3401  CB  GLU D 114      31.402  38.208  33.707  1.00 19.13           C
ATOM   3402  CG  GLU D 114      30.883  37.422  32.539  1.00 21.49           C
ATOM   3403  CD  GLU D 114      29.605  36.642  32.816  1.00 24.09           C
ATOM   3404  OE1 GLU D 114      29.017  36.697  33.897  1.00 26.51           O
ATOM   3405  OE2 GLU D 114      29.185  35.937  31.907  1.00 29.29           O
ATOM   3406  N   PHE D 115      33.204  39.041  35.990  1.00 13.99           N
ATOM   3407  CA  PHE D 115      33.464  39.892  37.125  1.00 12.83           C
ATOM   3408  C   PHE D 115      34.753  40.667  36.905  1.00 13.21           C
ATOM   3409  O   PHE D 115      34.827  41.855  37.193  1.00 14.99           O
ATOM   3410  CB  PHE D 115      33.650  39.018  38.359  1.00 10.89           C
ATOM   3411  CG  PHE D 115      33.982  39.867  39.569  1.00 11.83           C
ATOM   3412  CD1 PHE D 115      32.951  40.361  40.344  1.00 12.60           C
ATOM   3413  CD2 PHE D 115      35.296  40.133  39.917  1.00 14.96           C
ATOM   3414  CE1 PHE D 115      33.251  41.093  41.480  1.00 12.59           C
ATOM   3415  CE2 PHE D 115      35.605  40.892  41.033  1.00 13.04           C
ATOM   3416  CZ  PHE D 115      34.560  41.373  41.810  1.00 14.57           C
ATOM   3417  N   PHE D 116      35.833  40.025  36.477  1.00 15.07           N
ATOM   3418  CA  PHE D 116      37.102  40.718  36.297  1.00 13.94           C
ATOM   3419  C   PHE D 116      37.181  41.563  35.036  1.00 15.79           C
ATOM   3420  O   PHE D 116      38.014  42.455  34.965  1.00 16.79           O
ATOM   3421  CB  PHE D 116      38.273  39.775  36.373  1.00 13.55           C
ATOM   3422  CG  PHE D 116      38.548  39.261  37.759  1.00 10.27           C
ATOM   3423  CD1 PHE D 116      39.105  40.100  38.692  1.00 12.82           C
ATOM   3424  CD2 PHE D 116      38.143  37.990  38.132  1.00 11.47           C
ATOM   3425  CE1 PHE D 116      39.169  39.689  40.025  1.00 14.46           C
ATOM   3426  CE2 PHE D 116      38.216  37.584  39.457  1.00 10.67           C
ATOM   3427  CZ  PHE D 116      38.709  38.439  40.407  1.00 11.80           C
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Figure 8-68

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ATOM   3428  N   ARG D 117      36.361  41.405  34.011  1.00 16.57           N
ATOM   3429  CA  ARG D 117      36.293  42.421  32.990  1.00 20.64           C
ATOM   3430  C   ARG D 117      35.668  43.700  33.548  1.00 22.51           C
ATOM   3431  O   ARG D 117      36.089  44.803  33.174  1.00 23.89           O
ATOM   3432  CB  ARG D 117      35.446  41.879  31.860  1.00 26.52           C
ATOM   3433  CG  ARG D 117      35.518  42.709  30.598  1.00 31.58           C
ATOM   3434  CD  ARG D 117      34.496  42.146  29.640  1.00 35.05           C
ATOM   3435  NE  ARG D 117      34.394  43.021  28.483  1.00 38.58           N
ATOM   3436  CZ  ARG D 117      33.828  42.656  27.326  1.00 37.56           C
ATOM   3437  NH1 ARG D 117      33.169  41.506  27.170  1.00 33.95           N
ATOM   3438  NH2 ARG D 117      34.002  43.473  26.286  1.00 37.95           N
ATOM   3439  N   ILE D 118      34.656  43.594  34.445  1.00 22.03           N
ATOM   3440  CA  ILE D 118      34.052  44.753  35.121  1.00 19.63           C
ATOM   3441  C   ILE D 118      35.047  45.368  36.086  1.00 19.88           C
ATOM   3442  O   ILE D 118      35.183  46.586  36.085  1.00 23.21           O
ATOM   3443  CB  ILE D 118      32.781  44.357  35.874  1.00 20.68           C
ATOM   3444  CG1 ILE D 118      31.691  43.843  34.951  1.00 19.48           C
ATOM   3445  CG2 ILE D 118      32.255  45.562  36.619  1.00 20.52           C
ATOM   3446  CD1 ILE D 118      30.567  43.143  35.727  1.00 18.63           C
ATOM   3447  N   PHE D 119      35.741  44.577  36.908  1.00 16.07           N
ATOM   3448  CA  PHE D 119      36.853  45.059  37.683  1.00 15.72           C
ATOM   3449  C   PHE D 119      37.853  45.894  36.880  1.00 17.75           C
ATOM   3450  O   PHE D 119      38.208  47.006  37.267  1.00 20.22           O
ATOM   3451  CB  PHE D 119      37.545  43.866  38.359  1.00 12.02           C
ATOM   3452  CG  PHE D 119      38.822  44.222  39.100  1.00 13.89           C
ATOM   3453  CD1 PHE D 119      38.760  44.766  40.389  1.00 14.47           C
ATOM   3454  CD2 PHE D 119      40.057  44.030  38.492  1.00 10.48           C
ATOM   3455  CE1 PHE D 119      39.944  45.148  41.032  1.00 13.14           C
ATOM   3456  CE2 PHE D 119      41.219  44.387  39.149  1.00 10.95           C
ATOM   3457  CZ  PHE D 119      41.163  44.965  40.405  1.00 10.47           C
ATOM   3458  N   ASN D 120      38.349  45.343  35.779  1.00 18.18           N
ATOM   3459  CA  ASN D 120      39.325  45.994  34.955  1.00 18.15           C
ATOM   3460  C   ASN D 120      38.709  47.263  34.387  1.00 20.79           C
ATOM   3461  O   ASN D 120      39.348  48.303  34.408  1.00 22.36           O
ATOM   3462  CB  ASN D 120      39.805  45.078  33.812  1.00 18.05           C
ATOM   3463  CG  ASN D 120      40.849  44.026  34.137  1.00 17.71           C
ATOM   3464  OD1 ASN D 120      41.770  44.210  34.918  1.00 21.36           O
ATOM   3465  ND2 ASN D 120      40.765  42.860  33.538  1.00 17.03           N
ATOM   3466  N   ARG D 121      37.463  47.256  33.941  1.00 22.71           N
ATOM   3467  CA  ARG D 121      36.824  48.438  33.431  1.00 24.59           C
ATOM   3468  C   ARG D 121      36.703  49.523  34.494  1.00 27.41           C
ATOM   3469  O   ARG D 121      36.971  50.683  34.192  1.00 30.49           O
ATOM   3470  CB  ARG D 121      35.468  47.993  32.953  1.00 26.42           C
ATOM   3471  CG  ARG D 121      34.608  49.156  32.549  1.00 33.46           C
ATOM   3472  CD  ARG D 121      34.760  49.641  31.105  1.00 37.32           C
ATOM   3473  NE  ARG D 121      34.149  50.962  30.882  1.00 39.99           N
ATOM   3474  CZ  ARG D 121      32.836  51.217  31.020  1.00 39.01           C
ATOM   3475  NH1 ARG D 121      31.955  50.306  31.426  1.00 37.27           N
ATOM   3476  NH2 ARG D 121      32.392  52.439  30.747  1.00 40.47           N
ATOM   3477  N   SER D 122      36.364  49.186  35.754  1.00 28.07           N
ATOM   3478  CA  SER D 122      36.147  50.153  36.820  1.00 24.66           C
ATOM   3479  C   SER D 122      37.455  50.758  37.250  1.00 25.38           C
ATOM   3480  O   SER D 122      37.536  51.971  37.401  1.00 24.85           O
ATOM   3481  CB  SER D 122      35.452  49.505  37.983  1.00 20.76           C
ATOM   3482  OG  SER D 122      34.236  48.886  37.591  1.00 19.10           O
ATOM   3483  N   ILE D 123      38.513  49.954  37.389  1.00 28.58           N
ATOM   3484  CA  ILE D 123      39.853  50.468  37.718  1.00 31.03           C
ATOM   3485  C   ILE D 123      40.396  51.464  36.684  1.00 33.54           C
ATOM   3486  O   ILE D 123      40.998  52.471  37.040  1.00 33.54           O
ATOM   3487  CB  ILE D 123      40.821  49.267  38.041  1.00 31.69           C
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Figure 8-69

ATOM	3488	CG1	ILE	D	123	40.899	48.877	39.544	1.00	30.91	C
ATOM	3489	CG2	ILE	D	123	42.262	49.504	37.583	1.00	31.27	C
ATOM	3490	CD1	ILE	D	123	39.609	48.826	40.377	1.00	31.19	C
ATOM	3491	N	ASP	D	124	40.123	51.244	35.395	1.00	36.80	N
ATOM	3492	CA	ASP	D	124	40.562	52.125	34.333	1.00	38.72	C
ATOM	3493	C	ASP	D	124	39.846	53.455	34.353	1.00	39.18	C
ATOM	3494	O	ASP	D	124	40.487	54.491	34.186	1.00	39.94	O
ATOM	3495	CB	ASP	D	124	40.383	51.461	32.981	1.00	42.50	C
ATOM	3496	CG	ASP	D	124	40.847	52.342	31.828	1.00	47.69	C
ATOM	3497	OD1	ASP	D	124	42.058	52.554	31.646	1.00	50.62	O
ATOM	3498	OD2	ASP	D	124	39.972	52.837	31.116	1.00	51.18	O
ATOM	3499	N	ALA	D	125	38.538	53.440	34.590	1.00	39.43	N
ATOM	3500	CA	ALA	D	125	37.731	54.649	34.586	1.00	41.04	C
ATOM	3501	C	ALA	D	125	38.028	55.640	35.712	1.00	44.24	C
ATOM	3502	O	ALA	D	125	37.580	56.792	35.729	1.00	46.63	O
ATOM	3503	CB	ALA	D	125	36.289	54.232	34.688	1.00	37.89	C
ATOM	3504	N	PHE	D	126	38.795	55.189	36.693	1.00	47.55	N
ATOM	3505	CA	PHE	D	126	39.342	56.063	37.709	1.00	52.08	C
ATOM	3506	C	PHE	D	126	40.409	57.058	37.208	1.00	55.06	C
ATOM	3507	O	PHE	D	126	40.531	58.167	37.751	1.00	57.33	O
ATOM	3508	CB	PHE	D	126	39.877	55.182	38.838	1.00	51.90	C
ATOM	3509	CG	PHE	D	126	39.154	55.489	40.124	1.00	50.92	C
ATOM	3510	CD1	PHE	D	126	39.155	56.780	40.620	1.00	52.88	C
ATOM	3511	CD2	PHE	D	126	38.437	54.505	40.745	1.00	50.11	C
ATOM	3512	CE1	PHE	D	126	38.390	57.105	41.721	1.00	54.34	C
ATOM	3513	CE2	PHE	D	126	37.688	54.827	41.851	1.00	52.08	C
ATOM	3514	CZ	PHE	D	126	37.653	56.117	42.336	1.00	53.64	C
ATOM	3515	N	LYS	D	127	41.187	56.667	36.177	1.00	56.75	N
ATOM	3516	CA	LYS	D	127	42.055	57.566	35.420	1.00	57.29	C
ATOM	3517	C	LYS	D	127	41.257	58.229	34.273	1.00	58.91	C
ATOM	3518	O	LYS	D	127	41.376	57.826	33.098	1.00	60.03	O
ATOM	3519	CB	LYS	D	127	43.225	56.735	34.882	1.00	56.61	C
TER	3521		LYS	D	127						
HETATM	3522	CA	CA		1021	34.563	32.796	27.927	1.00	28.47	CA
HETATM	3523	CA	CA		1022	29.874	41.216	51.866	1.00	42.93	CA
HETATM	3524	CA	CA		1023	46.453	8.630	31.415	1.00	34.99	CA
HETATM	3525	OH2	1PE		1	18.016	39.096	31.870	1.00	54.04	O
HETATM	3526	C12	1PE		1	19.233	39.467	31.241	1.00	52.50	C
HETATM	3527	C22	1PE		1	20.344	39.764	32.285	1.00	52.87	C
HETATM	3528	OH3	1PE		1	21.455	40.455	31.657	1.00	50.81	O
HETATM	3529	C13	1PE		1	21.887	42.392	30.182	1.00	41.29	C
HETATM	3530	C23	1PE		1	20.971	41.737	31.213	1.00	45.45	C
HETATM	3531	OH4	1PE		1	23.085	42.870	30.757	1.00	37.80	O
HETATM	3532	C14	1PE		1	24.265	44.731	31.534	1.00	39.00	C
HETATM	3533	C24	1PE		1	22.866	44.120	31.391	1.00	35.49	C
HETATM	3534	OH5	1PE		1	25.158	43.676	31.917	1.00	39.07	O
HETATM	3535	C15	1PE		1	27.396	42.942	31.976	1.00	36.51	C
HETATM	3536	C25	1PE		1	26.476	44.138	32.222	1.00	37.63	C
HETATM	3537	OH6	1PE		1	26.797	41.817	32.602	1.00	37.94	O
HETATM	3538	C16	1PE		1	28.795	40.537	32.878	1.00	44.86	C
HETATM	3539	C26	1PE		1	27.405	40.589	32.251	1.00	38.90	C
HETATM	3540	OH7	1PE		1	29.817	40.999	31.987	1.00	53.59	O
HETATM	3541	O	HOH		1024	36.890	32.430	27.721	1.00	24.58	O
HETATM	3542	O	HOH		1025	35.049	30.934	29.322	1.00	27.97	O
HETATM	3543	O	HOH		1026	31.347	42.865	52.839	1.00	31.45	O
HETATM	3544	O	HOH		1027	44.819	10.251	32.056	1.00	31.08	O
HETATM	3545	O	HOH		1028	47.508	7.695	33.365	1.00	35.15	O
HETATM	3546	O	HOH		1029	48.695	9.256	30.957	1.00	29.22	O
HETATM	3547	O	HOH		1105	33.704	13.935	20.986	1.00	32.21	O
HETATM	3548	O	HOH		1106	22.707	17.800	13.006	1.00	51.74	O

Figure 8-70

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HETATM 3549  O   HOH  1107      25.589  22.952  23.068  1.00 38.86           O
HETATM 3550  O   HOH  1108      20.410  17.104  15.299  1.00 29.07           O
HETATM 3551  O   HOH  1109      26.763   8.355  29.315  1.00 19.21           O
HETATM 3552  O   HOH  1110      25.744  13.365  30.461  1.00 32.06           O
HETATM 3553  O   HOH  1111      27.532   6.721  32.848  1.00 38.65           O
HETATM 3554  O   HOH  1112      18.245  18.266  16.629  1.00 28.39           O
HETATM 3555  O   HOH  1113      23.260  14.366  29.164  1.00 21.00           O
HETATM 3556  O   HOH  1114      15.116  22.225  22.815  1.00 19.32           O
HETATM 3557  O   HOH  1115      15.033  21.355  35.696  1.00 38.95           O
HETATM 3558  O   HOH  1116      20.651   6.306  35.427  1.00 25.08           O
HETATM 3559  O   HOH  1117      15.267  18.912  37.475  1.00 41.62           O
HETATM 3560  O   HOH  1118      13.693  14.872  13.312  1.00 29.91           O
HETATM 3561  O   HOH  1119      10.257  20.310  28.411  1.00 19.75           O
HETATM 3562  O   HOH  1120      17.034   0.246  35.599  1.00 32.81           O
HETATM 3563  O   HOH  1121       6.051  17.933  31.202  1.00 21.61           O
HETATM 3564  O   HOH  1122       4.997  14.576  24.993  1.00 33.94           O
HETATM 3565  O   HOH  1123       0.916  19.643  30.618  1.00 37.91           O
HETATM 3566  O   HOH  1124       5.906  11.136  30.408  1.00 46.39           O
HETATM 3567  O   HOH  1125       6.559   5.604  30.508  1.00 37.39           O
HETATM 3568  O   HOH  1126       8.033   4.439  28.006  1.00 43.67           O
HETATM 3569  O   HOH  1127       5.753   3.756  33.445  1.00 43.48           O
HETATM 3570  O   HOH  1128      44.059  26.360  36.277  1.00 22.42           O
HETATM 3571  O   HOH  1129      34.421  31.639  20.635  1.00 57.58           O
HETATM 3572  O   HOH  1130      50.215  13.426  34.211  1.00 31.74           O
HETATM 3573  O   HOH  1132      22.455  45.496  39.519  1.00 46.16           O
HETATM 3574  O   HOH  1133      13.246  35.686   8.764  1.00 63.66           O
HETATM 3575  O   HOH  1134      34.029  21.538  54.154  1.00 48.71           O
HETATM 3576  O   HOH  1135      46.505  41.139  53.506  1.00 25.80           O
HETATM 3577  O   HOH  1136      14.868  40.514   7.810  1.00 46.95           O
HETATM 3578  O   HOH  1138      37.977  45.274  53.726  1.00 41.75           O
HETATM 3579  O   HOH  1139      10.511  41.610  30.508  1.00 54.06           O
HETATM 3580  O   HOH  1140      21.928  44.651  36.769  1.00 27.65           O
HETATM 3581  O   HOH  1141       9.657  38.390  31.085  1.00 36.52           O
HETATM 3582  O   HOH  1142      35.556  55.905  31.455  1.00 33.05           O
HETATM 3583  O   HOH  1143      52.337  31.433  47.975  1.00 42.15           O
HETATM 3584  O   HOH  1144      32.915  38.699  23.494  1.00 40.84           O
HETATM 3585  O   HOH  1145      29.548  21.469  24.434  1.00 44.50           O
HETATM 3586  O   HOH  1146      26.181  34.331  29.823  1.00 34.71           O
HETATM 3587  O   HOH  1147      39.069   5.943  33.085  1.00 53.70           O
HETATM 3588  O   HOH  1148      34.970  24.222  52.427  1.00 40.12           O
HETATM 3589  O   HOH  1149      59.825  24.478  48.580  1.00 40.98           O
HETATM 3590  O   HOH  1150      28.412  33.531  47.673  1.00 44.44           O
HETATM 3591  O   HOH  1151      25.454  33.933  32.960  1.00 35.88           O
HETATM 3592  O   HOH  1152      41.875  59.115  53.350  1.00 51.54           O
HETATM 3593  O   HOH  1153      45.977  17.661  29.654  1.00 48.44           O
HETATM 3594  O   HOH  1154      16.374  19.854  15.198  1.00 26.92           O
HETATM 3595  O   HOH  1156       2.909  45.550   9.710  1.00 33.50           O
HETATM 3596  O   HOH  1157      27.955  42.970  52.054  1.00 42.09           O
HETATM 3597  O   HOH  1158      18.671  28.692  31.947  1.00 31.92           O
HETATM 3598  O   HOH  1160      31.097  11.069  39.837  1.00 22.54           O
HETATM 3599  O   HOH  1161      24.551  47.693  13.911  1.00 39.92           O
HETATM 3600  O   HOH  1162      19.328  46.523  39.555  1.00 49.64           O
HETATM 3601  O   HOH  1163      14.463  28.577  32.747  1.00 33.62           O
HETATM 3602  O   HOH  1164      42.334  34.141  31.684  1.00 25.02           O
HETATM 3603  O   HOH  1165      26.640  35.518  34.853  1.00 25.40           O
HETATM 3604  O   HOH  1166      41.719  26.191  52.537  1.00 54.23           O
HETATM 3605  O   HOH  1167      11.799  43.370   8.564  1.00 42.64           O
HETATM 3606  O   HOH  1169      39.695  23.691  29.775  1.00 46.55           O
HETATM 3607  O   HOH  1170      25.519 -10.203  13.390  1.00 29.39           O
HETATM 3608  O   HOH  1172      15.639  30.378   9.410  1.00 35.98           O
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Figure 8-71

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HETATM 3609  O   HOH  1173      26.042  53.508  19.228  1.00 35.35           O
HETATM 3610  O   HOH  1174      16.723  43.317   9.437  1.00 70.54           O
HETATM 3611  O   HOH  1175      11.039  27.202  31.989  1.00 35.23           O
HETATM 3612  O   HOH  1176      26.492  54.880  14.660  1.00 45.35           O
HETATM 3613  O   HOH  1177      48.739   5.603  40.080  1.00 46.72           O
HETATM 3614  O   HOH  1179      38.452  10.611  56.410  1.00 33.18           O
HETATM 3615  O   HOH  1180      25.173  41.020  50.981  1.00 37.80           O
HETATM 3616  O   HOH  1181      26.009  21.500  26.306  1.00 37.33           O
HETATM 3617  O   HOH  1185      32.901  61.354  32.974  1.00 47.36           O
HETATM 3618  O   HOH  1186      49.199  44.404  48.616  1.00 55.72           O
HETATM 3619  O   HOH  1187      28.401  31.064  46.621  1.00 25.46           O
HETATM 3620  O   HOH  1189      50.488  34.252  43.662  1.00 27.11           O
HETATM 3621  O   HOH  1190      25.015  38.231  32.413  1.00 46.20           O
HETATM 3622  O   HOH  1191      13.328  45.647   6.880  1.00 50.19           O
HETATM 3623  O   HOH  1192       9.102  28.582  30.815  1.00 28.84           O
HETATM 3624  O   HOH  1194      16.216  53.125  18.778  1.00 20.19           O
HETATM 3625  O   HOH  1195      48.924  37.778  50.511  1.00 41.81           O
HETATM 3626  O   HOH  1196      29.151  29.120  42.414  1.00 25.51           O
HETATM 3627  O   HOH  1197      10.760  56.327  24.871  1.00 25.61           O
HETATM 3628  O   HOH  1198      19.161  31.540  33.429  1.00 41.50           O
HETATM 3629  O   HOH  1201      31.584  19.545  39.778  1.00 41.14           O
HETATM 3630  O   HOH  1202      31.499  33.130  31.243  1.00 30.94           O
HETATM 3631  O   HOH  1203      33.475  31.251  32.729  1.00 30.16           O
HETATM 3632  O   HOH  1204      25.323  26.251  24.066  1.00 29.38           O
HETATM 3633  O   HOH  1205      18.912  50.780  14.345  1.00 28.88           O
HETATM 3634  O   HOH  1206      28.562  46.055  22.818  1.00 37.71           O
HETATM 3635  O   HOH  1207      31.212  15.396  37.505  1.00 38.29           O
HETATM 3636  O   HOH  1208      21.188  13.368  44.376  1.00 22.37           O
HETATM 3637  O   HOH  1209      17.682  38.715  10.160  1.00 31.02           O
HETATM 3638  O   HOH  1210      50.214  11.867  37.111  1.00 50.09           O
HETATM 3639  O   HOH  1212      28.768  41.646  47.276  1.00 22.25           O
HETATM 3640  O   HOH  1214      49.993  18.233  34.806  1.00 44.55           O
HETATM 3641  O   HOH  1215      32.815  34.522  46.504  1.00 35.13           O
HETATM 3642  O   HOH  1216      39.893  28.328  41.896  1.00 12.01           O
HETATM 3643  O   HOH  1217      15.338  26.949  28.916  1.00 11.70           O
HETATM 3644  O   HOH  1218      35.548  32.617  33.681  1.00 18.33           O
HETATM 3645  O   HOH  1219      39.368  28.656  34.414  1.00 16.49           O
HETATM 3646  O   HOH  1220      10.631  22.205  16.485  1.00 23.48           O
HETATM 3647  O   HOH  1221      38.404  33.931  29.548  1.00 20.31           O
HETATM 3648  O   HOH  1222      29.170  43.940  45.652  1.00 17.85           O
HETATM 3649  O   HOH  1223      16.493  28.977  30.383  1.00 19.55           O
HETATM 3650  O   HOH  1224      50.201  26.750  43.278  1.00 23.76           O
HETATM 3651  O   HOH  1225      38.642  25.017  49.298  1.00 24.48           O
HETATM 3652  O   HOH  1226      22.132  37.260  38.648  1.00 21.90           O
HETATM 3653  O   HOH  1227      39.985  27.256  49.971  1.00 19.31           O
HETATM 3654  O   HOH  1228      46.680  26.589  41.727  1.00 24.34           O
HETATM 3655  O   HOH  1229      45.783  30.693  47.582  1.00 25.33           O
HETATM 3656  O   HOH  1230      37.132  23.521  50.764  1.00 25.39           O
HETATM 3657  O   HOH  1231      37.666  45.416  31.269  1.00 22.37           O
HETATM 3658  O   HOH  1232      12.017  34.217  29.751  1.00 24.35           O
HETATM 3659  O   HOH  1233      26.995  45.967  27.617  1.00 23.52           O
HETATM 3660  O   HOH  1234      26.536  25.536  28.250  1.00 29.21           O
HETATM 3661  O   HOH  1235      25.412  37.399  29.161  1.00 27.51           O
HETATM 3662  O   HOH  1236      37.339  31.390  35.413  1.00 25.38           O
HETATM 3663  O   HOH  1237      49.870  32.179  49.678  1.00 25.92           O
HETATM 3664  O   HOH  1238      22.061  39.616  17.387  1.00 15.04           O
HETATM 3665  O   HOH  1239      14.228  24.366  29.787  1.00 22.47           O
HETATM 3666  O   HOH  1240      23.022  47.566  29.327  1.00 39.50           O
HETATM 3667  O   HOH  1241      21.098  32.679  17.559  1.00 35.09           O
HETATM 3668  O   HOH  1242      23.864  37.449  16.707  1.00 37.28           O
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Figure 8-72

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HETATM 3669  O   HOH  1243      32.934  17.639  38.491  1.00 30.00           O
HETATM 3670  O   HOH  1244      30.081  39.275  47.475  1.00 27.25           O
HETATM 3671  O   HOH  1245      40.219  10.507  54.210  1.00 42.36           O
HETATM 3672  O   HOH  1246      20.198  57.839  14.584  1.00 26.12           O
HETATM 3673  O   HOH  1247      22.701  31.034  19.118  1.00 26.32           O
HETATM 3674  O   HOH  1248      50.529  25.000  51.117  1.00 16.36           O
HETATM 3675  O   HOH  1249      27.308  27.122  38.575  1.00 29.98           O
HETATM 3676  O   HOH  1250      41.664  46.630  31.018  1.00 29.42           O
HETATM 3677  O   HOH  1251      27.841  34.202  44.699  1.00 37.98           O
HETATM 3678  O   HOH  1252      28.946  26.204  44.341  1.00 51.94           O
HETATM 3679  O   HOH  1253      26.643  43.795  23.560  1.00 23.03           O
HETATM 3680  O   HOH  1254      52.894  25.886  44.095  1.00 33.52           O
HETATM 3681  O   HOH  1255      42.339  26.613  55.952  1.00 36.97           O
HETATM 3682  O   HOH  1256      48.804   2.432  50.876  1.00 36.59           O
HETATM 3683  O   HOH  1257      51.244  18.531  40.805  1.00 33.51           O
HETATM 3684  O   HOH  1260      49.903  39.828  48.137  1.00 44.77           O
HETATM 3685  O   HOH  1261      45.720   4.638  32.384  1.00 54.41           O
HETATM 3686  O   HOH  1262      32.871  29.567  30.088  1.00 39.72           O
HETATM 3687  O   HOH  1263      23.890  51.918  23.175  1.00 37.61           O
HETATM 3688  O   HOH  1264      13.550  26.049  31.905  1.00 33.45           O
HETATM 3689  O   HOH  1266      10.689  31.547  31.432  1.00 47.94           O
HETATM 3690  O   HOH  1269      26.086  -7.425  31.507  1.00 39.58           O
HETATM 3691  O   HOH  1271      22.022  54.673  22.853  1.00 37.03           O
HETATM 3692  O   HOH  1274      28.901  24.308  41.027  1.00 41.39           O
HETATM 3693  O   HOH  1276      45.609  -2.697  31.603  1.00 49.62           O
HETATM 3694  O   HOH  1277       9.649  26.708  34.475  1.00 36.02           O
HETATM 3695  O   HOH  1279      21.970   8.818  36.303  1.00 45.69           O
HETATM 3696  O   HOH  1280       7.956  56.039  27.031  1.00 55.41           O
HETATM 3697  O   HOH  1281      15.342  17.025  12.461  1.00 55.13           O
HETATM 3698  O   HOH  1284      12.862  44.437   3.810  1.00 49.95           O
HETATM 3699  O   HOH  1286      34.675  64.010  47.159  1.00 47.97           O
HETATM 3700  O   HOH  1287      41.049  11.857  30.681  1.00 29.94           O
HETATM 3701  O   HOH  1288      34.457  19.302  55.855  1.00 47.88           O
HETATM 3702  O   HOH  1289      28.546  31.433  28.564  1.00 47.71           O
HETATM 3703  O   HOH  1291      33.220  60.645  39.548  1.00 52.03           O
HETATM 3704  O   HOH  1292      30.910  54.312  27.471  1.00 48.06           O
HETATM 3705  O   HOH  1293      23.058  27.656  32.358  1.00 45.02           O
HETATM 3706  O   HOH  1294      28.377  27.865  25.772  1.00 37.73           O
HETATM 3707  O   HOH  1295      17.851  13.033  47.051  1.00 31.43           O
HETATM 3708  O   HOH  1297      22.435  24.151  33.420  1.00 39.38           O
HETATM 3709  O   HOH  1298      29.292  20.833  37.423  1.00 52.78           O
HETATM 3710  O   HOH  1299      26.196  40.554  47.655  1.00 52.83           O
HETATM 3711  O   HOH  1300       6.687  28.384  34.247  1.00 45.71           O
HETATM 3712  O   HOH  1303      41.624   1.272  27.661  1.00 61.55           O
HETATM 3713  O   HOH  1306      24.865  48.368  49.108  1.00 53.05           O
HETATM 3714  O   HOH  1308      43.375  33.196  54.115  1.00 54.68           O
HETATM 3715  O   HOH  1309      24.941  16.106  28.105  1.00 27.22           O
HETATM 3716  O   HOH  1310      48.767  36.362  53.067  1.00 39.18           O
HETATM 3717  O   HOH  1311       0.897  25.934  24.841  1.00 47.80           O
HETATM 3718  O   HOH  1312      41.531  54.883  30.082  1.00 37.92           O
HETATM 3719  O   HOH  1315      32.370  19.055  31.177  1.00 43.71           O
HETATM 3720  O   HOH  1316      19.469  15.072  45.662  1.00 48.16           O
HETATM 3721  O   HOH  1321      10.144  48.734   5.731  1.00 39.11           O
HETATM 3722  O   HOH  1322      29.076  56.977  42.203  1.00 46.38           O
HETATM 3723  O   HOH  1326      42.727   8.091  54.610  1.00 56.42           O
HETATM 3724  O   HOH  1330      41.316  20.071  29.052  1.00 39.86           O
HETATM 3725  O   HOH  1331      16.596  27.837  34.825  1.00 50.15           O
HETATM 3726  O   HOH  1332      19.903  45.162  47.256  1.00 52.33           O
HETATM 3727  O   HOH  1333      40.238  -8.133  39.062  1.00 41.11           O
HETATM 3728  O   HOH  1335      32.007  37.168  46.170  1.00 43.84           O
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Figure 8-73

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HETATM 3729  O   HOH  1337       8.866  32.982  29.638  1.00 51.57           O
HETATM 3730  O   HOH  1339      35.650  46.023  29.211  1.00 40.99           O
HETATM 3731  O   HOH  1340      52.825  32.335  38.756  1.00 50.57           O
HETATM 3732  O   HOH  1341      36.938  51.807  31.314  1.00 45.30           O
HETATM 3733  O   HOH  1342      18.790  42.705  33.580  1.00 43.47           O
HETATM 3734  O   HOH  1344      22.819  36.661  11.619  1.00 46.70           O
HETATM 3735  O   HOH  1345      19.465  28.669  34.714  1.00 39.89           O
HETATM 3736  O   HOH  1347      40.179  23.790  53.530  1.00 47.43           O
HETATM 3737  O   HOH  1353       3.487  36.484  13.806  1.00 40.41           O
HETATM 3738  O   HOH  1360      31.223   4.884  34.089  1.00 30.96           O
HETATM 3739  O   HOH  1361      19.647   3.819  14.444  1.00 26.16           O
HETATM 3740  O   HOH  1364      12.171  -3.712  34.829  1.00 52.07           O
HETATM 3741  O   HOH  1366      14.715  10.503  15.414  1.00 47.98           O
HETATM 3742  O   HOH  1370       3.284  18.073  30.684  1.00 39.22           O
HETATM 3743  O   HOH  1371      16.114  12.267  13.222  1.00 41.79           O
HETATM 3744  O   HOH  1374      26.710 -10.158  28.570  1.00 46.72           O
HETATM 3745  O   HOH  1376      13.842   2.095  17.391  1.00 51.23           O
HETATM 3746  O   HOH  1377      23.624  18.176  26.993  1.00 46.55           O
HETATM 3747  O   HOH  1378      17.679   9.897  14.906  1.00 29.42           O
HETATM 3748  O   HOH  1380      21.173  -2.881  15.825  1.00 44.25           O
HETATM 3749  O   HOH  1381      25.990   6.184  14.411  1.00 40.98           O
HETATM 3750  O   HOH  1382      25.475   8.938  15.031  1.00 40.93           O
HETATM 3751  O   HOH  1384      27.045  17.549  12.911  1.00 44.46           O
HETATM 3752  O   HOH  1387      15.174  -5.506  13.111  1.00 43.09           O
HETATM 3753  O   HOH  1388       3.093  25.580  28.841  1.00 47.33           O
HETATM 3754  O   HOH  1389      43.833  14.822  32.665  1.00 30.09           O
HETATM 3755  O   HOH  1390      27.283   3.257  16.277  1.00 28.50           O
HETATM 3756  O   HOH  1391      31.590   8.283  17.790  1.00 31.43           O
HETATM 3757  O   HOH  1392      28.183   8.699  15.618  1.00 37.69           O
HETATM 3758  O   HOH  1393      24.599   3.854  15.072  1.00 40.30           O
HETATM 3759  O   HOH  1404      39.148  30.436  32.035  1.00 17.64           O
HETATM 3760  O   HOH  1405       0.837  22.245  22.324  1.00 55.83           O
HETATM 3761  O   HOH  1406      29.799  34.134  27.910  1.00 28.75           O
HETATM 3762  O   HOH  1407      18.445   6.222  44.059  1.00 53.71           O
HETATM 3763  O   HOH  1409      30.392  39.323  25.039  1.00 34.89           O
HETATM 3764  O   HOH  1410      18.490   9.793  47.086  1.00 48.51           O
HETATM 3765  O   HOH  1411      13.220  32.748   8.629  1.00 49.26           O
HETATM 3766  O   HOH  1412      49.361  20.100  32.438  1.00 43.65           O
HETATM 3767  O   HOH  1414      51.855  33.864  41.242  1.00 64.26           O
HETATM 3768  O   HOH  1418      47.727  41.100  41.717  1.00 35.47           O
HETATM 3769  O   HOH  1419      24.466  54.548  43.747  1.00 53.28           O
HETATM 3770  O   HOH  1420       5.934  30.983   8.318  1.00 45.39           O
HETATM 3771  O   HOH  1421      32.399  -4.433  42.259  1.00 41.31           O
HETATM 3772  O   HOH  1422       3.024  40.996  27.927  1.00 42.40           O
HETATM 3773  O   HOH  1424      36.321  -0.489  35.913  1.00 41.12           O
HETATM 3774  O   HOH  1428      16.200  42.165   4.789  1.00 62.98           O
HETATM 3775  O   HOH  1429       4.930  40.213  24.269  1.00 53.41           O
HETATM 3776  O   HOH  1430       7.506   9.248  13.243  1.00 51.74           O
HETATM 3777  O   HOH  1434      16.093  51.978  11.936  1.00 39.24           O
HETATM 3778  O   HOH  1437      32.063  21.866  31.547  1.00 49.87           O
HETATM 3779  O   HOH  1438      54.621  26.247  29.147  1.00 48.62           O
HETATM 3780  O   HOH  1440       4.318  19.369   8.919  1.00 47.53           O
HETATM 3781  O   HOH  1441       5.136   2.358  29.831  1.00 44.25           O
HETATM 3782  O   HOH  1443       2.076  24.174  15.211  1.00 53.91           O
HETATM 3783  O   HOH  1444      15.474  42.729  30.690  1.00 38.63           O
HETATM 3784  O   HOH  1446      34.955   9.442  53.656  1.00 51.40           O
HETATM 3785  O   HOH  1447      28.597  17.387  31.041  1.00 40.53           O
HETATM 3786  O   HOH  1454      34.884  -9.534  12.912  1.00 33.84           O
HETATM 3787  O   HOH  1455      56.971  31.610  49.136  1.00 44.36           O
HETATM 3788  O   HOH  1456      29.676  11.548  53.175  1.00 41.64           O
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Figure 8-74

```
HETATM 3789  O   HOH  1457      46.713  47.217  35.996  1.00 51.75           O
HETATM 3790  O   HOH  1458      22.556   3.172  12.871  1.00 35.99           O
HETATM 3791  O   HOH  1459      42.572  42.347  52.583  1.00 55.24           O
HETATM 3792  O   HOH  1461       0.573  13.064  16.484  1.00 44.57           O
HETATM 3793  O   HOH  1462      50.467   6.260  32.228  1.00 46.40           O
HETATM 3794  O   HOH  1463       6.167  47.337   5.349  1.00 53.27           O
HETATM 3795  O   HOH  1464      24.604  -9.866  26.249  1.00 43.72           O
HETATM 3796  O   HOH  1466      22.806  17.220  45.236  1.00 61.41           O
HETATM 3797  O   HOH  1506      25.441  49.608  19.993  1.00 33.89           O
HETATM 3798  O   HOH  1507      39.709  -9.399  16.482  1.00 30.44           O
HETATM 3799  O   HOH  1509       9.926  24.411  36.529  1.00 37.21           O
HETATM 3800  O   HOH  1515      34.731  28.232  28.355  1.00 37.81           O
HETATM 3801  O   HOH  1518      44.323  37.583  28.523  1.00 44.08           O
HETATM 3802  O   HOH  1519      30.194  -0.768  45.229  1.00 40.11           O
HETATM 3803  O   HOH  1521      42.425  48.375  34.242  1.00 50.42           O
HETATM 3804  O   HOH  1523      12.185   2.224  34.335  1.00 56.22           O
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CONECT 1118 1116 1119
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Figure 8-75

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CONECT 1119 1118 1120 1122
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CONECT 1126 1120 1127
CONECT 1177 1176 1874
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CONECT 2831 2825 2832
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Figure 8-76

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CONECT 2895 2894 2896 2901
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CONECT 3535 3536 3537
CONECT 3536 3534 3535
CONECT 3537 3535 3539
CONECT 3538 3539 3540
CONECT 3539 3537 3538
CONECT 3540 3538
CONECT 3541 3522
CONECT 3542 3522
CONECT 3544 3524
CONECT 3545 3524
CONECT 3546 3524
MASTER      301    0   16   19    8    0    0   27 3796    4  147   84
END
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Figure 9

```
submitted:
HETATM 4233  O   HOH  1021      36.890  32.430  27.721  1.00 24.58
HETATM 4234  O   HOH  1021      35.049  30.934  29.322  1.00 27.97
HETATM 4236  O   HOH  1022      31.347  42.865  52.839  1.00 31.45
HETATM 4238  O   HOH  1023      44.819  10.251  32.056  1.00 31.08
HETATM 4239  O   HOH  1023      47.508   7.695  33.365  1.00 35.15
HETATM 4240  O   HOH  1023      48.695   9.256  30.957  1.00 29.22


to this:
HETATM 4233  O   HOH  1021      36.890  32.430  27.721  1.00 24.58
HETATM 4234  O   HOH  1022      35.049  30.934  29.322  1.00 27.97
HETATM 4236  O   HOH  1023      31.347  42.865  52.839  1.00 31.45
HETATM 4238  O   HOH  1024      44.819  10.251  32.056  1.00 31.08
HETATM 4239  O   HOH  1025      47.508   7.695  33.365  1.00 35.15
HETATM 4240  O   HOH  1026      48.695   9.256  30.957  1.00 29.22


The LINKs are:

LINK         CA    CA  1021                 O   HOH  1024
LINK         CA    CA  1021                 O   HOH  1025
LINK         CA    CA  1023                 O   HOH  1027
LINK         CA    CA  1023                 O   HOH  1028
LINK         CA    CA  1023                 O   HOH  1029
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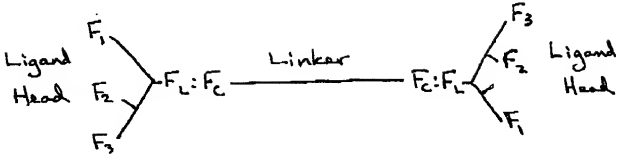
Figure 10

A. General model



B. Embodiment of the ligand head as an oligopeptide

$F_1 - X_n - F_L(Cys) - X_m - F_2 - X_p - F_3$

DECLARATION AND POWER OF ATTORNEY

As a below-named inventor, I hereby declare that:

My residence, post office address, and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

the specification of which:
(check one)

X *is attached hereto.*

X *was filed on* June 29, 2000 *as*

Application Serial No. _____

and was amended _____
(if applicable)

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the U.S. Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119 (a)-(d) or Section 365(b) of any foreign application(s) for patent or inventor's certificate, or Section 365(a) of any PCT International Application which designated at least one country other than the United States, listed below. I have also identified below any foreign application for patent or inventor's certificate, or PCT International Application having a filing date before that of the earliest application from which priority is claimed:

Prior Foreign Application(s)			*Priority Claimed*	
Number	*Country*	*Filing Date*	*Yes*	*No*
N/A				

I hereby claim the benefit under Title 35, United States Code, Section 119(e) of any United States provisional application(s) listed below:

Provisional Application No.	*Filing Date*	*Status*
N/A		

I hereby claim the benefit under Title 35, United States Code, Section 120 of any United States Application(s), or Section 365(c) of any PCT International Application(s) designating the United States listed below. Insofar as this application discloses and claims subject matter in addition to that disclosed in any such prior Application in the manner provided by the first paragraph of Title 35, United States Code, Section 112, I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56, which became available between the filing date(s) of such prior Application(s) and the national or PCT international filing date of this application:

Application Serial No.	*Filing Date*	*Status*
N/A		

And I hereby appoint

John P. White (Reg. No. 28,678); Christopher C. Dunham (Reg. No. 22,031); Norman H. Zivin (Reg. No. 25,385); Jay H. Maioli (Reg. No. 27,213); William E. Pelton (Reg. No. 25,702); Robert D. Katz (Reg. No. 30,141); Peter J. Phillips (Reg. No. 29,691); Wendy E. Miller (Reg. No. 35,615); Richard S. Milner (Reg. No. 33,970); Robert T. Maldonado (Reg. 38,232); Paul Teng (40,837); Richard F. Jaworski (Reg. No. 33,515); Elizabeth M. Wieckowski (Reg. No. 42,226); Pedro C. Fernandez (Reg. No. 41,741); Gary J. Gershik (Reg. No. 39,992); Jane M. Love (Reg. No. 42,812); Spencer H. Schneider (Reg. No. 45,923) and Raymond A. Diperna (Reg. No. 44,063).

and each of them, all c/o Cooper & Dunham LLP, 1185 Avenue of the Americas, New York, New York 10036, my attorneys, each with full power of substitution and revocation, to prosecute this application, to make alterations and amendments therein, to receive the patent, to transact all business in the Patent and Trademark Office connected therewith and to file any International Applications which are based thereon under the provisions of the Patent Cooperation Treaty.

Please address all communications, and direct all telephone calls, regarding this application to

John P. White, Esq. *Reg. No.* 28,678
Cooper & Dunham LLP
1185 Avenue of the Americas
New York, New York 10036
Tel. (212) 278-0400

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon

Full name of sole or first joint inventor Wayne A. Hendrickson

Inventor's signature _____

Citizenship _____ *Date of signature* _____

Residence _____

Post Office Address _____

_____

Full name of joint inventor (if any) Xuliang Jiang

Inventor's signature _____

Citizenship _____ *Date of signature* _____

Residence _____

Post Office Address _____

_____

Full name of joint inventor (if any) Keith E. Langley

Inventor's signature _____

Citizenship _____ *Date of signature* _____

Residence _____

Post Office Address _____

_____

Full name of joint inventor (if any) Rashid Syed

*Inventor's signature*_____

*Citizenship*_____ *Date of signature*_____

*Residence*_____

*Post Office Address*_____

_____

Full name of joint inventor (if any) Yueh-Rong Ann Hsu

*Inventor's signature*_____

*Citizenship*_____ *Date of signature*_____

*Residence*_____

*Post Office Address*_____

_____

*Full name of joint inventor (if any)*_____

*Inventor's signature*_____

*Citizenship*_____ *Date of signature*_____

*Residence*_____

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SEQUENCE LISTING

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Jiang, Xuliang
Langley, Keith E
Syed, Rashid
Hsu, Yueh-Rong Ann

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         35                  40                  45

Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser
     50                  55                  60

Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
 65                  70                  75                  80

Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser Lys
                 85                  90                  95

Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro
            100                 105                 110
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             20                  25                  30

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
         35                  40                  45

Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
     50                  55                  60

Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
 65                  70                  75                  80

Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
                85                  90                  95

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            100                 105                 110

Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
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Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr Arg
50 55 60

Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile
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Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu
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35 40 45

Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln
50 55 60

```
Gly Leu Arg Gly Ser Leu Thr Lys Ile Lys Gly Pro Leu Thr Met Met
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Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser Cys
                85                  90                  95

Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp
            100                 105                 110

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            20                  25                  30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Tyr Met Pro Lys Lys
        35                  40                  45

Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro
    50                  55                  60

Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
 65                  70                  75                  80

Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys
                85                  90                  95

Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
            100                 105                 110

Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile
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Ser Thr Leu Thr
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Phe Gln Gly Ile Gly Thr Leu Glu Ser Gln Thr Val Gln Gly Gly Thr
50 55 60

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Gly Gln Lys Lys Lys Cys Gly Glu Glu Arg Arg Arg Val Asn Gln Phe
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35 40 45

Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser
50 55 60

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Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
 65                  70                  75                  80

Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser Lys
                85                  90                  95

Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro
            100                 105                 110

Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp
        115                 120                 125

Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu
    130                 135                 140

Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu
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            20                  25                  30

Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met
        35                  40                  45

Val Ile Gln Leu Ser Leu Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser
    50                  55                  60

Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly
65                  70                  75                  80

Lys Ile Val Asp Asp Leu Val Leu Cys Met Glu Glu Asn Ala Pro Lys
                85                  90                  95

Asn Ile Lys Glu Ser Pro Lys Arg Pro Glu Thr Arg Ser Phe Thr Pro
            100                 105                 110
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Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp
        115                 120                 125

Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu
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            20                  25                  30

Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met
        35                  40                  45

Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser
    50                  55                  60

Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly
65                  70                  75                  80

Lys Ile Val Asp Asp Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys
                85                  90                  95

Asn Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro
            100                 105                 110

Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp
        115                 120                 125

Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu
    130                 135                 140

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Asn Val Lys Lys Ala Pro Lys Ser Pro Glu Leu Arg Leu Phe Thr Pro
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Leu Pro Pro Val Ala
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